

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000993_191713_c3_904	2170	5942	1109	3696	1884	6.9e-195

Description

gp: [GI:e286140:g4775551] [LN: SACTORF13] [AC: Y09928] [OR: *Staphylococcus aureus*] [DB: genpept-bct1] [DE: *S. aureus* CTORF1365, partial.] [NT: CTORF1365] [LE: <1] [RE: >3982] [DI: direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000993_19565876_c3_915	2171	5943	201	66		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000993_1960937_c3_964	2172	5944	177	58	228	5.1e-19

Description

gp: [GI:g1022726] [LN: SHU35635] [AC: U35635] [PN: unknown] [OR: *Staphylococcus haemolyticus*] [SR: *Staphylococcus haemolyticus* strain=Y176] [DB: genpept-bct1] [DE: *Staphylococcus haemolyticus* IS1272 ORF1 and ORF2 genes, completecds.] [NT: ORF1] [LE: 1101] [RE: 1922] [DI: complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000993_19742842_c2_769	2173	5945	849	282	776	4.4e-77

Description

pir: [LN: C70040] [AC: C70040] [PN: plant-metabolite dehydrogenase homolog yvgN] [GN: yvgN] [CL: aldehyde reductase] [OR: *Bacillus subtilis*] [DB: pir2] >gp: [GI: e1249784:g2832788] [LN: BS43KBDNA] [AC: AJ223978] [PN: putative reductase protein, YvgN] [GN: yvgN] [OR: *Bacillus subtilis*] [DB: genpept-bct1] [DE: *Bacillus subtilis* 42.7kB DNA fragment from yvsA to yvqA.] [LE: 646] [RE: 1476] [DI: direct] >gp: [GI: e1186028:g2635853] [LN: BSUB0018] [AC: Z99121: AL009126] [GN: yvgN] [FN: unknown] [OR: *Bacillus subtilis*] [DB: genpept-bct1] [DE: *Bacillus subtilis* complete genome (section 18 of 21): from 3399551 to 3609060.] [NT: alternate gene name: yvsB; similar to] [LE: 26261] [RE: 27091] [DI: complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000993_19770437_c2_830	2174	5946	1332	443	1018	9.9e-103

Description

pir: [LN: A69998] [AC: A69998] [PN: hypothetical protein ytoI] [GN: ytoI] [OR: *Bacillus subtilis*] [DB: pir2] >gp: [GI: e1184176:g2635392] [LN: BSUB0015] [AC: Z99118: AL009126] [GN: ytoI] [FN: unknown] [OR: *Bacillus subtilis*] [DB: genpept-bct1] [DE: *Bacillus subtilis* complete genome (section 15 of 21): from 2795131 to 3013540.] [LE: 201244] [RE: 202563] [DI: complement] >gp: [GI: g2293258] [LN: AF008220] [AC: AF008220] [PN: YtoI] [GN: ytoI] [OR: *Bacillus subtilis*] [DB: genpept-bct2] [DE: *Bacillus subtilis* rrnB-dnaB genomic region.] [NT: similarity with hypothetical protein 3 from] [LE: 180504] [RE: 181823] [DI: direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000993_1991325_f3_469	2175	5947	219	72		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000993_19922162_c3_857	2176	5948	1161	386	527	1.1e-50

Description

gp:[GI:g3688818] [LN:AF084104] [AC:AF084104] [PN:hypothetical protein] [OR:Bacillus firmus] [DB:genpept-bct2] [DE:Bacillus firmus AcsA (acsA) gene, partial cds; SspA (sspA), hypothetical protein, maltose transporter ATP-binding protein(malK), leucine-rich protein transcriptional regulator (lrpR), hypothetical proteins, ABC transporter ATP-binding protein (natC), NatA (natA), NatB (natB), and hypothetical protein genes, completecds; and SpoIIJJ (spoIIJJ) gene, partial cds.] [NT:Orf10; similar to hypothetical protein YheB from] [LE:5845] [RE:6957] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000993_1992943_f3_561	2177	5949	747	248	104	2.3e-05

Description

gp:[GI:g160225] [LN:PFACSPI] [AC:M18821] [PN:circumsporozoite protein] [GN:CSP] [OR:Plasmodium yoelii] [SR:Plasmodium yoelii (strain 17X NL) DNA] [DB:genpept-inv1] [DE:Plasmodium yoelii circumsporozoite protein (CSP) gene, 5' end.] [NT:precursor] [LE:1] [RE:>420] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000993_20365892_c1_731	2178	5950	150	49		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000993_2051502_f2_250	2179	5951	159	52		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000993_20706557_c3_860	2180	5952	1254	417	592	1.4e-57

Description

pir:[LN:A69819] [AC:A69819] [PN:probable phosphoesterase, yhaO] [GN:yhaO] [CL:unassigned probable phosphoesterases: phosphoesterase core homology] [OR:Bacillus subtilis] [EC:3.1.---] [DB:pir2] >gp:[GI:e1182993:g2633327] [LN:BSUB0006] [AC:Z99109:AL009126] [GN:yhaO] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 6 of 21): from 999501 to 1209940.] [NT:similar to hypothetical proteins] [LE:64822] [RE:66048] [DI:direct] >gp:[GI:e324934:g2226129] [LN:BSY14078] [AC:Y14078] [PN:Hypothetical protein] [GN:yhaO] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis 8.7 Kb chromosomal DNA: downstream glyB-prsAregion.] [NT:similarity to exonuclease sbcD from Escherichia] [LE:4292] [RE:5518] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000993_20834812_f2_339	2181	5953	306	101	86	0.0039

Description

pir:[LN:S77632] [AC:S77632:S52761] [PN:probable integrase] [GN:int] [OR:Staphylococcus aureus phage phi-13] [DB:pir2] >gp:[GI:g758229] [LN:PHI13INT] [AC:X82312] [PN:integrase] [GN:int] [FN:integration of phi-13 in S.aureus genome] [OR:Bacteriophage phi-13] [DB:genpept-phg] [DE:Bacteriophage phi-13 integrase gene.] [LE:461] [RE:1498] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000993_20901713_c3_939	2182	5954	1707	568	613	8.2e-60
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Description

pir:[LN:G70002] [AC:G70002] [PN:hypothetical protein ytwP] [GN:ytwP] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1185834:g2635445] [LN:BSUB0016] [AC:Z99119:AL009126] [GN:ytwP] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.] [LE:31035] [RE:32723] [DI:complement] >gp:[GI:g2293228] [LN:AF008220] [AC:AF008220] [PN:YtwP] [GN:ytwP] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis rrnB-dnaB genomic region.] [NT:similarity to fcrA protein precursor from] [LE:147704] [RE:149392] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000993_20947781_f2_348	2183	5955	126	41		
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000993_2115812_f2_222	2184	5956	1113	370	843	3.5e-84
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Description

pir:[LN:G69869] [AC:G69869] [PN:Xaa-Pro dipeptidase homolog ykvY] [GN:ykvY] [CL:X-Pro aminopeptidase] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1184976:g2633757] [LN:BSUB0008] [AC:Z99111:AL009126] [GN:ykvY] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.] [NT:similar to Xaa-Pro dipeptidase] [LE:58367] [RE:59458] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000993_2117077_f3_536	2185	5957	366	121	195	1.6e-15
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Description

pir:[LN:A70341] [AC:A70341] [PN:conserved hypothetical protein aq\_449] [GN:aq\_449] [CL:hypothetical protein MJ1523] [OR:Aquifex aeolicus] [DB:pir2] >gp:[GI:g2983116] [LN:AE000690] [AC:AE000690:AE000657] [PN:hypothetical protein] [GN:aq\_449] [OR:Aquifex aeolicus] [DB:genpept-bct2] [DE:Aquifex aeolicus section 22 of 109 of the complete genome.] [LE:10789] [RE:11163] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000993_2126250_f2_305	2186	5958	210	69		
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000993_21491462_c1_722	2187	5959	1161	386	1188	9.6e-121

Description

sp: [LN:CISZ\_BACSU] [AC:P39120:O34435] [GN:CITZ:CITA2] [OR:BACILLUS SUBTILIS] [EC:4.1.3.7] [DE:CITRATE SYNTHASE II,] [SP:P39120:O34435] [DB:swissprot] >pir: [LN:G69600] [AC:G69600:I40381] [PN:citrate synthase II,] [GN:citz] [CL:citrate (si)-synthase] [OR:Bacillus subtilis] [EC:4.1.3.-] [DB:pir2] >gp: [GI:e1184163:g2635379] [LN:BSUB0015] [AC:Z99118:AL009126] [PN:citrate synthase II] [GN:citz] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:4.1.3.7] [DE:Bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.] [NT:alternate gene name: citA2] [SP:P39120] [LE:185094] [RE:186212] [DI:complement] >gp: [GI:g2293267] [LN:AF008220] [AC:AF008220] [PN:citrate synthase subunit II] [GN:citz] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis rrnB-dnaB genomic region.] [LE:196855] [RE:197973] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000993_21520887_c2_781	2188	5960	135	44		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000993_21522010_f2_331	2189	5961	1725	574	2393	2.0e-248

Description

sp: [LN:PPCK\_STAAU] [AC:P51065] [GN:PCKA] [OR:STAPHYLOCOCCUS AUREUS] [EC:4.1.1.49] [DE:PHOSPHOENOLPYRUVATE CARBOXYKINASE [ATP,] [SP:P51065] [DB:swissprot] >gp: [GI:g1255262] [LN:SAU51133] [AC:U51133] [PN:phosphoenolpyruvate carboxykinase] [GN:pcka] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:Staphylococcus aureus phosphoenolpyruvate carboxykinase (pcka)gene, complete cds.] [LE:160] [RE:1752] [DI:direct] >gp: [GI:g860732] [LN:STAPEPCK] [AC:L42943] [PN:phosphoenolpyruvate carboxykinase] [GN:pckA] [OR:Staphylococcus aureus] [DB:genpept-bct1] [EC:4.1.1.32] [DE:Staphylococcus aureus (clone KIN50) phosphoenolpyruvatecarboxykinase (pckA) gene, complete cds.] [NT:PEPCK; homologue] [LE:409] [RE:2001] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000993_21523400_f2_356	2190	5962	162	53		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000993_21645967_f3_575	2191	5963	993	330	368	7.5e-34

Description

sp: [LN:PRSA\_BACSU] [AC:P24327] [GN:PRSA] [OR:BACILLUS SUBTILIS] [DE:PROTEIN EXPORT PROTEIN PRSA PRECURSOR] [SP:P24327] [DB:swissprot] >pir: [LN:S15269] [AC:S15269:I40003:H69682] [PN:post-translocation molecular chaperone prsA:33K lipoprotein prsA] [GN:prsA] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:g39782] [LN:BS33KDA] [AC:X57271:S67658] [PN:33kDa lipoprotein] [GN:prsA] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B. subtilis prsA gene for a 33kDa lipoprotein.] [SP:P24327] [LE:63] [RE:941] [DI:direct] >gp: [GI:e1182997:g2633331] [LN:BSUB0006] [AC:Z99109:AL009126] [PN:molecular chaperonin] [GN:prsA] [FN:essential for the stability of secreted] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 6 of 21): from 999501 to 1209940.] [SP:P24327] [LE:70340] [RE:71218] [DI:complement] >gp: [GI:e325181:g2226124] [LN:BSY14077] [AC:Y14077] [PN:33kDa lipoprotein] [GN:prsA] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis 10.6 Kb chromosomal DNA: glyB-prsA region.] [NT:See Swiss Prot P24327] [SP:P24327] [LE:9695] [RE:10573] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000993_2189718_f3_412	2192	5964	1371	456	1309	1.4e-133

Description

sp: [LN:CYCA\_ECOLI] [AC:P39312] [GN:CYCA:DAGA] [OR:ESCHERICHIA COLI] [DE:D-SERINE/D-ALANINE/GLYCINE TRANSPORTER] [SP:P39312] [DB:swissprot] >pir: [LN:S56433] [AC:S56433:C65232] [PN:d-serine/d-alanine/glycine transporter] [GN:cycA] [CL:arginine permease] [OR:Escherichia coli] [DB:pir2] >gp: [GI:g537049] [LN:ECOUW93] [AC:U14003] [OR:Escherichia coli] [DB:genpept-bct1] [DE:Escherichia coli K-12 chromosomal region from 92.8 to 00.1 minutes.] [NT:ORF\_o470] [LE:120696] [RE:122108] [DI:direct] >gp: [GI:g1790653] [LN:AE000492] [AC:AE000492:U00096] [PN:transport of D-alanine, D-serine, and glycine] [GN:cycA] [FN:transport; Transport of small molecules: Amino] [OR:Escherichia coli] [DB:genpept-bct2] [DE:Escherichia coli K-12 MG1655 section 382 of 400 of the complete genome.] [NT:o470; 100 pct identical amino acid sequence and] [LE:2436] [RE:3848] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000993_22078331_f3_564	2193	5965	252	83		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000993_22164757_f2_244	2194	5966	132	43		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000993_22271932_c1_651	2195	5967	132	43		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000993_22277327_c3_968	2196	5968	1371	456	496	2.0e-47

Description

sp: [LN:DNAB\_BACSU] [AC:P07908] [GN:DNAB] [OR:BACILLUS SUBTILIS] [DE:REPLICATION INITIATION AND MEMBRANE ATTACHMENT PROTEIN] [SP:P07908] [DB:swissprot] >pir: [LN:B26580] [AC:B26580:A24720:A69617] [PN:chromosome replication initiation / membrane attachment protein dnaB:dnaB protein] [GN:dnaB] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:g142863] [LN:BACDNAB] [AC:M15183] [PN:replication initiation protein] [GN:dnaB] [OR:Bacillus subtilis] [SR:Bacillus subtilis (sub\_strain PY79, strain W168) DNA] [DB:genpept-bct1] [DE:B.subtilis dnaB gene, encoding the replication initiation and membrane attachment protein, complete cds, clone pdnaB12.] [NT:The part of the protein encoded by 634-693 binds to] [LE:397] [RE:1815] [DI:direct] >gp: [GI:e1184148:g2635364] [LN:BSUB0015] [AC:Z99118:AL009126] [PN:membrane attachment protein] [GN:dnaB] [FN:initiation of chromosome replication (DNA)] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 15 of 21): from 2795131 to 3013540.] [LE:168092] [RE:169510] [DI:complement] >gp: [GI:e1165285:g1769995] [LN:BSZ75208] [AC:Z75208] [PN:replication initiation protein] [GN:dnaB] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis genomic sequence 89009bp.] [NT:the part of the protein encoded by 634-693 binds to] [SP:P07908] [LE:397] [RE:1815] [DI:direct] >gp: [GI:g2293280] [LN:AF008220] [AC:AF008220] [PN:DnaB] [GN:dnaB] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis rrnB-dnaB genomic region.] [LE:213557] [RE:214975] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000993_22391432_f3_562	2197	5969	525	174	288	2.3e-25

Description

pir: [LN:S77632] [AC:S77632:S52761] [PN:probable integrase] [GN:int] [OR:Staphylococcus aureus phage phi-13] [DB:pir2] >gp: [GI:g758229] [LN:PHI13INT] [AC:X82312] [PN:integrase] [GN:int] [FN:integration of phi-13 in S.aureus genome] [OR:Bacteriophage phi-13] [DB:genpept-phg] [DE:Bacteriophage phi-13 integrase gene.] [LE:461] [RE:1498] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000993_22459692_f1_125	2198	5970	201	66		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000993_22664125_c2_832	2199	5971	165	54		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000993_23438837_f3_600	2200	5972	132	43		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000993_23468812_f1_141	2201	5973	129	42		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000993_23485443_c1_709	2202	5974	1239	412	931	1.6e-93

Description

sp: [LN:THII\_BACSU] [AC:O34595] [GN:THII] [OR:BACILLUS SUBTILIS] [DE:PROBABLE THIAMIN BIOSYNTHESIS PROTEIN THII] [SP:O34595] [DB:swissprot] >pir: [LN:E69988] [AC:E69988] [PN:conserved hypothetical protein ytbJ] [GN:ytbJ] [CL:Mycoplasma genitalium hypothetical protein MG372] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1185831:g2635442] [LN:BSUB0016] [AC:Z99119:AL009126] [GN:ytbJ] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.] [NT:similar to hypothetical proteins] [SP:O34595] [LE:27183] [RE:28259] [DI:complement] >gp: [GI:g2293230] [LN:AF008220] [AC:AF008220] [PN:YtbJ] [GN:ytbJ] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis rrnB-dnaB genomic region.] [NT:similar to hypothetical protein MG372 from M.] [LE:152168] [RE:153244] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000993_23489090_c2_835	2203	5975	1038	345	1033	2.5e-104

Description

sp: [LN:K6PF\_BACSU] [AC:O34529] [GN:PFKA:PFK] [OR:BACILLUS SUBTILIS] [EC:2.7.1.11] [DE:(PHOSPHOHEXOKINASE)] [SP:O34529] [DB:swissprot] >pir: [LN:A69675] [AC:A69675] [PN:6-phosphofructokinase pfk] [GN:pfk] [CL:6-phosphofructokinase:6-phosphofructokinase 1 homology] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1184168:g2635384] [LN:BSUB0015] [AC:Z99118:AL009126] [PN:6-phosphofructokinase] [GN:pfk] [FN:glycolysis] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:2.7.1.11] [DE:Bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.] [SP:O34529] [LE:190531] [RE:191490] [DI:complement] >gp: [GI:g2293264] [LN:AF008220] [AC:AF008220] [PN:6-phosphofructokinase] [GN:pfk] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis rrnB-dnaB genomic region.] [LE:191577] [RE:192536] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000993_23555302_f2_233	2204	5976	387	128	91	0.00083

Description

gp: [GI:e1363147:g4127385] [LN:APR011678] [AC:AJ011678] [PN:immunodominant protein] [OR:Apple proliferation phytoplasma] [DB:genpept-bct1] [DE:Apple proliferation phytoplasma immunodominant protein gene, strainAT.] [LE:885] [RE:1382] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000993_23601713_c3_894	2205	5977	1194	397	1108	2.9e-112

Description

sp: [LN:GCH2\_BACAM] [AC:P51695] [GN:RIBA] [OR:BACILLUS AMYLOLIQUEFACIENS] [EC:3.5.4.25] [DE:PHOSPHATE SYNTHASE (DHBP SYNTHASE)] [SP:P51695] [DB:swissprot] >gp: [GI:e223994:g1212775] [LN:BARIBGENS] [AC:X95955] [PN:3,4-dihydroxy-2-butanone 4-phosphate synthase] [GN:ribA] [OR:Bacillus amyloliquefaciens] [DB:genpept-bct1] [DE:B.amyloliquefaciens ribB, ribG, ribA, ribH & ribT genes.] [NT:GTP cyclohydrolase II] [SP:P51695] [LE:2411] [RE:3607] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000993_23603375_f2_219	2206	5978	417	138	139	1.4e-09

Description

sp: [LN:Y577\_METJA] [AC:Q57997] [GN:MJ0577] [OR:METHANOCOCCUS JANNASCHII] [DE:PROTEIN MJ0577] [SP:Q57997] [DB:swissprot] >pir: [LN:A64372] [AC:A64372] [PN:hypothetical protein homolog MJ0577] [CL:Escherichia coli ybdQ protein] [OR:Methanococcus jannaschii] [DB:pir2] [MP:FOR512975-513463] >gp: [GI:g1591284] [LN:U67506] [AC:U67506:L77117] [PN:conserved hypothetical protein] [GN:MJ0577] [OR:Methanococcus jannaschii] [DB:genpept-bct2] [DE:Methanococcus jannaschii section 48 of 150 of the complete genome.] [NT:similar to SP:P42297 PID:603780 PID:849027] [LE:8204] [RE:8692] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000993_2362587_f2_321	2207	5979	150	49		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000993_23651567_c3_961	2208	5980	888	295	387	5.2e-41

Description

gp: [GI:d1025814:g2897751] [LN:AB008520] [AC:AB008520] [GN:mutM] [OR:Thermus thermophilus] [SR:Thermus thermophilus (strain:HB8) DNA] [DB:genpept-bct1] [DE:Thermus thermophilus MutM gene, complete cds.] [LE:297] [RE:1100] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000993_23694052_f2_359	2209	5981	603	200	82	0.0040

Description

pir: [LN:E69818] [AC:E69818] [PN:hypothetical protein yhAK] [GN:yhAK] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1182998:g2633332] [LN:BSUB0006] [AC:Z99109:AL009126] [GN:yhAK] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 6 of 21): from 999501 to 1209940.] [LE:72018] [RE:72272] [DI:complement] >gp: [GI:e324957:g2226123] [LN:BSY14077] [AC:Y14077] [PN:Hypothetical protein] [GN:yhAK] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis 10.6 Kb chromosomal DNA: glyB-prsA region.] [LE:8641] [RE:8895] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000993_23710885_f2_167	2210	5982	147	48	76	0.027

Description

pir: [LN:S72289] [AC:S72289] [PN:ribosomal protein L2] [GN:rpl2] [OR:plastid Plasmodium falciparum] [DB:pir2] >gp: [GI:e220178:g1171595] [LN:PFCOMPIRB] [AC:X95276] [GN:rpl2] [OR:Plasmodium falciparum] [SR:malaria parasite P. falciparum] [DB:genpept-inv1] [DE:P. falciparum complete gene map of plastid-like DNA (IR-B).] [LE:2799] [RE:3536] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000993_2380342_c2_741	2211	5983	636	211	463	6.4e-44

Description

pir:[LN:F69824] [AC:F69824] [PN:two-component response regulator [YhcY] homolog yhcZ] [GN:yhcZ] [CL:regulatory protein comA:response regulator homology] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1182922:g2633256] [LN:BSUB0005] [AC:Z99108:AL009126] [GN:yhcZ] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 5 of 21): from 802821 to 1011250.] [NT:similar to two-component response regulator [YhcY]] [LE:206441] [RE:207085] [DI:direct] >gp:[GI:e1182934:g2633268] [LN:BSUB0006] [AC:Z99109:AL009126] [GN:yhcZ] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 6 of 21): from 999501 to 1209940.] [NT:similar to two-component response regulator [YhcY]] [LE:9761] [RE:10405] [DI:direct] >gp:[GI:e324945:g2226141] [LN:BSY14079] [AC:Y14079] [PN:hypothetical protein] [GN:yhcZ] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis chromosomal DNA, region 75 degrees: glpPFKdoperon and downstream.] [NT:similarity to the transcriptional regulator degU] [LE:9409] [RE:10053] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000993_2383253_c1_635	2212	5984	198	65		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000993_23984787_c3_924	2213	5985	1011	336	1404	1.2e-143

Description

sp:[LN:CCPA\_STAXY] [AC:Q56194] [GN:CCPA] [OR:STAPHYLOCOCCUS XYLOSUS] [DE:PROBABLE CATABOLITE CONTROL PROTEIN A] [SP:Q56194] [DB:swissprot] >gp:[GI:e220318:g1177685] [LN:SXCCPA] [AC:X95439] [GN:ccpA] [OR:Staphylococcus xylosus] [DB:genpept-bct1] [DE:S.xylosus aroA, ccpA, acuC and acuA genes.] [SP:Q56194] [LE:1305] [RE:2294] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000993_24017890_c2_843	2214	5986	1428	476	1242	1.8e-126

Description

sp:[LN:LYSP\_ECOLI] [AC:P25737] [GN:LYSP:CADR] [OR:ESCHERICHIA COLI] [DE:LYSINE-SPECIFIC PERMEASE] [SP:P25737] [DB:swissprot]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000993_24020250_c1_654	2215	5987	882	293	551	6.5e-52

Description

gp:[GI:e1295630:g3184134] [LN:SSAASPROT] [AC:AJ000007] [PN:AAS surface protein] [GN:aas] [OR:Staphylococcus saprophyticus] [DB:genpept-bct1] [DE:Staphylococcus saprophyticus aas gene.] [LE:203] [RE:4594] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000993_24025463_c1_620	2216	5988	2952	983	1357	1.2e-138

Description

gp:[GI:g710421] [LN:SAU21636] [AC:U21636] [PN:unknown] [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus cmp-binding-factor 1 (cbf1) and ORF X genes, complete cds.] [NT:ORF X] [LE:52] [RE:1158] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000993_24226543_c1_704	2217	5989	783	260	365	1.6e-33

Description

pir:[LN:E69827] [AC:E69827] [PN:glycerophosphodiester phosphodiesterase homolog yhdW] [GN:yhdW] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1182963:g2633297] [LN:BSUB0006] [AC:Z99109:AL009126] [GN:yhdW] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 6 of 21): from 999501 to 1209940.] [NT:similar to glycerophosphodiester phosphodiesterase] [LE:37668] [RE:38399] [DI:complement] >gp:[GI:e1191883:g2226218] [LN:BSY14082] [AC:Y14082] [PN:hypothetical protein] [GN:yhdW] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis chromosomal DNA, region 72 to 75 degrees: spoVRto sspB.] [NT:Similarity to glycerol diester phosphodiesterase] [LE:24316] [RE:25047] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000993_2426312_f1_103	2218	5990	135	44		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000993_24272568_c2_782	2219	5991	147	48		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000993_2428950_c3_844	2220	5992	444	147	227	6.6e-19

Description

gp:[GI:g1022725] [LN:SHU35635] [AC:U35635] [PN:unknown] [OR:Staphylococcus haemolyticus] [SR:Staphylococcus haemolyticus strain=Y176] [DB:genpept-bct1] [DE:Staphylococcus haemolyticus IS1272 ORF1 and ORF2 genes, completecds.] [NT:ORF2] [LE:394] [RE:1083] [DI:complement] >gp:[GI:g295162] [LN:STAMECRA] [AC:L14017] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus (strain COL) DNA] [DB:genpept-bct1] [DE:Staphylococcus aureus methicillin-resistance protein (mecR) geneand unknown ORF, complete cds.] [NT:unknown ORF1; putative] [LE:1492] [RE:2181] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000993_24296925_f3_534	2221	5993	552	183	127	6.2e-08

Description

gp:[GI:e184374:g2104803] [LN:CBDNAPTCG] [AC:X87972] [GN:P-21] [OR:Clostridium botulinum] [DB:genpept-bct1] [DE:C. botulinum progenitor toxin complex genes.] [LE:2337] [RE:2882] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000993_24307677_c2_772	2222	5994	144	47		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000993_24334563_c2_789	2223	5995	453	150	109	1.5e-05

Description

gp: [GI:e1492342:g5262792] [LN:ATT13K14] [AC:AL080282] [PN:putative protein] [GN:T13K14.180] [OR:Arabidopsis thaliana] [SR:thale cress] [DB:genpept] [DE:Arabidopsis thaliana DNA chromosome 4, BAC clone T13K14 (ESSAproject).] [NT:similarity to desiccation-related protein,] [LE:67362:67832] [RE:67502:68491] [DI:directJoin]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000993_24337750_c3_913	2224	5996	852	283	1238	4.8e-126

Description

sp: [LN:DAAA\_STAHA] [AC:P54694] [GN:DAT] [OR:STAPHYLOCOCCUS HAEMOLYTICUS] [EC:2.6.1.21] [DE:TRANSAMINASE] [SP:P54694] [DB:swissprot] >gp: [GI:g517475] [LN:SHU12238] [AC:U12238] [PN:D-amino acid transaminase] [GN:dat] [OR:Staphylococcus haemolyticus] [DB:genpept-bct1] [DE:Staphylococcus haemolyticus Y176 D-amino acid transaminase (dat) gene, complete cds.] [LE:216] [RE:1064] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000993_24407577_c1_724	2225	5997	738	245	833	4.0e-83

Description

sp: [LN:PHOP\_BACSU] [AC:P13792] [GN:PHOP] [OR:BACILLUS SUBTILIS] [DE:PHOP] [SP:P13792] [DB:swissprot] >gp: [GI:g40056] [LN:BSPHOPDNA] [AC:X67676] [GN:phoP] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis phoP gene.] [SP:P13792] [LE:199] [RE:921] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000993_24407765_c1_710	2226	5998	795	264	413	1.3e-38

Description

sp: [LN:YCB9\_PSEDE] [AC:P29942] [OR:PSEUDOMONAS DENITRIFICANS] [DE:HYPOTHETICAL 27.4 KD PROTEIN IN COBO 3'REGION (ORF9)] [SP:P29942] [DB:swissprot] >pir: [LN:I38164] [AC:I38164] [PN:hypothetical protein 9] [OR:Pseudomonas sp.] [DB:pir2] >gp: [GI:g551929] [LN:PSECOPGEN] [AC:M62866] [OR:Pseudomonas denitrificans] [SR:Pseudomonas denitrificans (strain SC510) DNA] [DB:genpept-bct1] [DE:P.denitrificans cobN, cobO, cobP, cobQ, cobW, and ORF6-9 genes,complete cds.] [NT:ORF9] [LE:12364] [RE:13149] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000993_24409803_c1_633	2227	5999	123	40	81	0.019

Description

pir: [LN:S75730] [AC:S75730:S50064] [PN:8-amino-7-oxononanoate synthase, :7-keto-8-aminopalargonic acid synthetase:protein slr0917:7-keto-8-aminopalargonic acid synthetase:protein slr0917] [GN:bioF] [CL:5-aminolevulinate synthase] [OR:Synechocystis sp.] [SR:PCC 6803, , PCC 6803] [SR:PCC 6803, ] [EC:2.3.1.47] [DB:pir2] >gp: [GI:d1011116:g1673311] [LN:SYCSLLE] [AC:D64003:AB001339] [PN:7-keto-8-aminopalargonic acid synthetase] [GN:bioF] [OR:Synechocystis sp.] [SR:Synechocystis sp. (strain:PCC6803) DNA] [DB:genpept-bct1] [DE:Synechocystis sp. PCC6803 complete genome, 22/27, 2755703-2868766.] [NT:ORF\_ID:slr0917] [LE:35986] [RE:37299] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000993_24417252_c3_902	2228	6000	1248	415	1038	7.5e-105

Description

pir:[LN:F70001] [AC:F70001] [PN:multidrug resistance protein homolog yttB] [GN:yttB] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1185908:g2635519] [LN:BSUB0016] [AC:Z99119:AL009126] [GN:yttB] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.] [NT:similar to multidrug resistance protein] [LE:108543] [RE:109736] [DI:complement] >gp:[GI:g2293179] [LN:AF008220] [AC:AF008220] [PN:YttB] [GN:yttB] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis rrnB-dnaB genomic region.] [NT:similarity to tetracycline resistance protein from] [LE:70691] [RE:71884] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000993_24428760_f3_509	2229	6001	129	42		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000993_24475377_f3_537	2230	6002	159	52		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000993_24490702_c1_616	2231	6003	405	134	74	0.011

Description

sp:[LN:Y70A\_METJA] [AC:P81311] [GN:MJ0703.1] [OR:METHANOCOCCUS JANNASCHII] [DE:HYPOTHETICAL PROTEIN MJ0703.1] [SP:P81311] [DB:swissprot] >gp:[GI:g2826311] [LN:U67517] [AC:U67517:L77117] [PN:M. jannaschii predicted coding region MJ0703.1] [GN:MJ0703.1] [OR:Methanococcus jannaschii] [DB:genpept-bct2] [DE:Methanococcus jannaschii section 59 of 150 of the complete genome.] [NT:Brute Force ORF; identified by GeneMark; putative] [LE:94] [RE:402] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000993_24492130_f1_70	2232	6004	123	40		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000993_24508552_c3_971	2233	6005	1953	650	2471	1.1e-256

Description

sp: [LN:SYT1\_BACSU] [AC:P18255:P06570] [GN:THRS:THRSV] [OR:BACILLUS SUBTILIS] [EC:6.1.1.3] [DE:(THRRS)] [SP:P18255:P06570] [DB:swissprot] >pir:[LN:YSBST1] [AC:B37770:E24720:B69723] [PN:threonine--tRNA ligase,, major (thrS):threonyl-tRNA synthetase] [GN:thrS:thrSv] [CL:threonine--tRNA ligase] [OR:Bacillus subtilis] [EC:6.1.1.3] [DB:pir1] [MP:250 (degrees)] >gp:[GI:g143766] [LN:BACTRNASB] [AC:M36594] [OR:Bacillus subtilis] [SR:B.subtilis (strain 168) vegetative form DNA] [DB:genpept-bct1] [DE:B.subtilis threonyl-tRNA synthetase (thrSv) gene, complete cds.] [NT:(thrSv) (EC 6.1.1.3)] [LE:365] [RE:2296] [DI:direct] >gp:[GI:e1184144:g2635360] [LN:BSUB0015] [AC:Z99118:AL009126] [PN:threonyl-tRNA synthetase] [GN:thrS] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:6.1.1.3] [DE:Bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.] [SP:P18255] [LE:163202] [RE:165133] [DI:complement] >gp:[GI:e1165290:g1769999] [LN:BSZ75208] [AC:Z75208] [PN:threonyl-tRNA-synthetase] [GN:thrS] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:6.1.1.3] [DE:B.subtilis genomic sequence 89009bp.] [NT:thrs (111-180); Major threonyl-tRNA synthetase] [SP:P18255] [LE:4774] [RE:6705] [DI:direct] >gp:[GI:g2293284] [LN:AF008220] [AC:AF008220] [PN:threonine tRNA synthetase] [GN:thrS] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis rrnB-dnaB genomic region.] [LE:217934] [RE:219865] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000993_24609676_c2_773	2234	6006	471	156	72	0.030

Description

sp: [LN:NULM\_DASNO] [AC:O21333] [GN:MTND4L:ND4L:NADH4L] [OR:DASYPUS NOVEMCINCTUS] [SR:,NINE-BANDED ARMADILLO] [EC:1.6.5.3] [DE:NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4L,] [SP:O21333] [DB:swissprot] >gp:[GI:e311022:g2252509] [LN:MTDNCOMGN] [AC:Y11832] [GN:NADH4L] [OR:Mitochondrion Dasypus novemcinctus] [SR:nine-banded armadillo] [DB:genpept-mam] [DE:D.novemcinctus complete mitochondrial genome.] [SP:O21333] [LE:9903] [RE:10199] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000993_24662915_c3_960	2235	6007	2718	905	2572	2.1e-267

Description

sp: [LN:DPO1\_BACSU] [AC:O34996] [GN:POLA] [OR:BACILLUS SUBTILIS] [EC:2.7.7.7] [DE:DNA POLYMERASE I, (POL I)] [SP:O34996] [DB:swissprot] >pir:[LN:E69680] [AC:E69680] [PN:DNA polymerase I polA] [GN:polA] [CL:DNA-directed DNA polymerase I] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1184158:g2635374] [LN:BSUB0015] [AC:Z99118:AL009126] [PN:DNA polymerase I] [GN:polA] [FN:replication and DNA repair] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:2.7.7.7] [DE:Bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.] [SP:O34996] [LE:177125] [RE:179767] [DI:complement] >gp:[GI:g2293272] [LN:AF008220] [AC:AF008220] [PN:DNA-polymerase I] [GN:polA] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis rrnB-dnaB genomic region.] [LE:203300] [RE:205942] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000993_24692338_c3_895	2236	6008	474	157	540	4.5e-52

Description

sp: [LN:RISB\_BACAM] [AC:Q44681] [GN:RIBH] [OR:BACILLUS AMYLOLIQUEFACIENS] [EC:2.5.1.9] [DE:(LUMAZINE SYNTHASE) (RIBOFLAVIN SYNTHASE BETA CHAIN)] [SP:Q44681] [DB:swissprot] >gp:[GI:e223995:g1212776] [LN:BARIBGENS] [AC:X95955] [PN:lumazine synthase (b-subunit)] [GN:ribH] [OR:Bacillus amyloliquefaciens] [DB:genpept-bct1] [DE:B.amyloliquefaciens ribB, ribG, ribA, ribH & ribT genes.] [SP:Q44681] [LE:3639] [RE:4103] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000993_24720291_c2_322	2237	6009	498	165		

Description

NO-HIT

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000993_24726077_c3_965	2238	6010	1026	341	1088	3.8e-110

Description

sp: [LN:G3P2\_BACSU] [AC:034425] [GN:GAPB] [OR:BACILLUS SUBTILIS] [EC:1.2.1.12] [DE:GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE 2, (GAPDH)] [SP:O34425] [DB:swissprot] >pir: [LN:G69628] [AC:G69628] [PN:glyceraldehyde-3-phosphate dehydrogenase, gapB] [GN:gapB] [CL:glyceraldehyde-3-phosphate dehydrogenase] [OR:Bacillus subtilis] [EC:1.2.1.12] [DB:pir2] >gp: [GI:e1184151:g2635367] [LN:BSUB0015] [AC:Z99118:AL009126] [PN:glyceraldehyde-3-phosphate dehydrogenase] [GN:gapB] [FN:glycolysis] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:1.2.1.12] [DE:Bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.] [SP:O34425] [LE:170976] [RE:171998] [DI:complement] >gp: [GI:g2293277] [LN:AF008220] [AC:AF008220] [PN:glyceraldehyde-3-P-dehydrogenase] [GN:gapB] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis rrnB-dnaB genomic region.] [LE:211069] [RE:212091] [DI:direct]

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000993_24740701_c3_903	2239	6011	2508	835	3293	0.0

Description

sp: [LN:SYL\_BACSU] [AC:P36430:O34465] [GN:LEUS] [OR:BACILLUS SUBTILIS] [EC:6.1.1.4] [DE:LEUCYL-TRNA SYNTHETASE, (LEUCINE--TRNA LIGASE) (LEURS)] [SP:P36430:O34465] [DB:swissprot] >pir: [LN:D69650] [AC:D69650:A41882] [PN:leucine--tRNA ligase, leucyl-tRNA synthetase] [GN:leuS] [CL:leucine--tRNA ligase] [OR:Bacillus subtilis] [EC:6.1.1.4] [DB:pir2] >gp: [GI:e1185905:g2635516] [LN:BSUB0016] [AC:Z99119:AL009126] [PN:leucyl-tRNA synthetase] [GN:leuS] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:6.1.1.4] [DE:Bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.] [SP:P36430] [LE:103940] [RE:106354] [DI:complement] >gp: [GI:g2293181] [LN:AF008220] [AC:AF008220] [PN:leucine tRNA synthetase] [GN:leuS] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis rrnB-dnaB genomic region.] [LE:74073] [RE:76487] [DI:direct]

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000993_24744077_c2_739	2240	6012	183	60	74	0.011

Description

pir: [LN:B60608] [AC:B60608] [PN:myosin heavy chain] [CL:myosin heavy chain:myosin motor domain homology] [OR:Schistosoma mansoni] [DB:pir2]

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000993_24797177_c1_689	2241	6013	3534	1177	1450	1.7e-148

Description

pir:[LN:C69999] [AC:C69999] [PN:DNA translocase stage III sporulation prot homolog ytpT] [GN:ytpT] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1185853:g2635464] [LN:BSUB0016] [AC:Z99119:AL009126] [GN:ytpT] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.] [NT:similar to DNA translocase stage III sporulation] [LE:51038] [RE:53146] [DI:complement] >gp:[GI:g2293215] [LN:AF008220] [AC:AF008220] [PN:YtpT] [GN:ytpT] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis rrnB-dnaB genomic region.] [NT:strong similarity to FtsK of E. coli and SpoIIIE of] [LE:127280] [RE:129388] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000993_24853437_c1_661	2242	6014	831	276	423	1.1e-39

Description

pir:[LN:D69998] [AC:D69998] [PN:lysophospholipase homolog ytpA] [GN:ytpA] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1185924:g2635535] [LN:BSUB0016] [AC:Z99119:AL009126] [GN:ytpA] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.] [NT:similar to lysophospholipase] [LE:123973] [RE:124752] [DI:complement] >gp:[GI:g2293167] [LN:AF008220] [AC:AF008220] [PN:probable lysophospholipase] [GN:ytpA] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis rrnB-dnaB genomic region.] [LE:55675] [RE:56454] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000993_2538252_c2_752	2243	6015	981	326	988	1.5e-99

Description

sp:[LN:HEMZ\_BACSU] [AC:P32396] [GN:HEMH:HEMF] [OR:BACILLUS SUBTILIS] [EC:4.99.1.1] [DE:SYNTHETASE] [SP:P32396] [DB:swissprot] >pir:[LN:C47045] [AC:C47045:H69639] [PN:ferrochelatase, hemH] [GN:hemH] [OR:Bacillus subtilis] [EC:4.99.1.1] [DB:pir2] >gp:[GI:g143044] [LN:BACHEMEHY] [AC:M97208] [PN:ferrochelatase] [GN:hemH] [FN:iron is inserted into protoporphyrin IX giving] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain W168) DNA] [DB:genpept-bct1] [EC:4.99.1.1] [DE:Bacillus subtilis penicillin binding protein 1A (ponA) gene; uroporphyrinogen decarboxylase (hemE) gene; ferrochelatase (hemH) gene complete cds, (hemY) gene, complete cds; ORFA, complete cds; ORFB 5' end.] [LE:3038] [RE:3970] [DI:direct] >gp:[GI:e1183015:g2633349] [LN:BSUB0006] [AC:Z99109:AL009126] [PN:ferrochelatase] [GN:hemH] [FN:incorporation of iron into protoporphyrin IX] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:4.99.1.1] [DE:Bacillus subtilis complete genome (section 6 of 21): from 999501 to 1209940.] [NT:alternate gene name: hemF] [SP:P32396] [LE:87223] [RE:88155] [DI:direct] >gp:[GI:e1191886:g2226231] [LN:BSY14083] [AC:Y14083] [PN:Ferrochelatase (EC 4.99.1.1); incorporation of] [GN:hemH] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis chromosomal DNA, region 76-78 degrees: between gB-aprE.] [NT:see Swiss Prot P32396; HEMZ\_BACSU.] [SP:P32396] [LE:7082] [RE:8014] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000993_25398425_c2_824	2244	6016	1167	388	731	2.6e-72
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Description

pir:[LN:F69666] [AC:F69666] [PN:NifS protein homolog nifZ] [GN:nifZ] [CL:nitrogen fixation protein nifS] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1185832:g2635443] [LN:BSUB0016] [AC:Z99119:AL009126] [PN:NifS protein homolog] [GN:nifZ] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.] [LE:28263] [RE:29408] [DI:complement] >gp:[GI:g2293229] [LN:AF008220] [AC:AF008220] [PN:NifS2] [GN:nifS2] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis rrnB-dnaB genomic region.] [NT:similar to R.sphaeroides nitrogenase stabilizer] [LE:151019] [RE:152164] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000993_25476375_c2_813	2245	6017	135	44		
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000993_2548537_c1_703	2246	6018	222	73		
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000993_25586632_c2_759	2247	6019	135	44		
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000993_25665878_c1_683	2248	6020	1665	554	1014	2.6e-102
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Description

pir:[LN:G69992] [AC:G69992] [PN:spore cortex protein homolog ytgP] [GN:ytgP] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1185878:g2635489] [LN:BSUB0016] [AC:Z99119:AL009126] [GN:ytgP] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.] [NT:similar to spore cortex protein] [LE:74841] [RE:76475] [DI:complement] >gp:[GI:g2293198] [LN:AF008220] [AC:AF008220] [PN:YtgP] [GN:ytgP] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis rrnB-dnaB genomic region.] [NT:similar to SpoVB protein from B. subtilis] [LE:103951] [RE:105585] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000993_25667217_c3_962	2249	6021	627	208	405	9.0e-38

Description

sp: [LN:YTAG\_BACSU] [AC:O34932] [GN:YTAG] [OR:BACILLUS SUBTILIS] [DE:HYPOTHETICAL 22.0 KD PROTEIN IN GAPB-MUTM INTERGENIC REGION] [SP:O34932] [DB:swissprot] >pir: [LN:A69988] [AC:A69988] [PN:conserved hypothetical protein ytaG] [GN:ytaG] [CL:conserved hypothetical protein YDR196c] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1184155:g2635371] [LN:BSUB0015] [AC:Z99118:AL009126] [GN:ytaG] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.] [NT:similar to hypothetical proteins] [SP:O34932] [LE:174866] [RE:175459] [DI:complement] >gp: [GI:g2293275] [LN:AF008220] [AC:AF008220] [PN:YtaG] [GN:ytaG] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis rrnB-dnaB genomic region.] [NT:similar to hypothetical protein HI0890 from H.] [LE:207608] [RE:208201] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000993_25972087_c3_846	2250	6022	147	48		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000993_26175952_f3_532	2251	6023	258	85		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000993_26181551_c2_834	2252	6024	948	315	1016	1.6e-102

Description

sp: [LN:ACCA\_BACSU] [AC:O34847] [GN:ACCA] [OR:BACILLUS SUBTILIS] [EC:6.4.1.2] [DE:(EC 6.4.1.2)] [SP:O34847] [DB:swissprot] >pir: [LN:G69580] [AC:G69580] [PN:acetyl-CoA carboxylase,, carboxyltransferase alpha chain] [GN:accA] [CL:acetyl-CoA carboxylase, carboxyltransferase alpha chain] [OR:Bacillus subtilis] [EC:6.4.1.2] [DB:pir2] >gp: [GI:e1184169:g2635385] [LN:BSUB0015] [AC:Z99118:AL009126] [PN:acetyl CoA carboxylase (alpha subunit)] [GN:accA] [FN:long-chain fatty acid biosynthesis] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.] [SP:O34847] [LE:191674] [RE:192651] [DI:complement] >gp: [GI:g2293263] [LN:AF008220] [AC:AF008220] [PN:acetyl-CoA carboxylase subunit] [GN:accA] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis rrnB-dnaB genomic region.] [LE:190416] [RE:191393] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000993_26188891_f1_29	2253	6025	210	69	75	0.012

Description

pir: [LN:S58751] [AC:S58751] [PN:NADH dehydrogenase (ubiquinone), chain 3] [CL:NADH dehydrogenase (ubiquinone) chain 3] [OR:mitochondrion Hansenula wingei] [EC:1.6.5.3] [DB:pir2]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000993_26259686_f3_450	2254	6026	1242	413	801	9.8e-80

Description

pir: [LN:A69643] [AC:A69643] [PN:serine proteinase Do, heat-shock protein htrA] [GN:htrA] [CL:proteinase hhOB] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1181491:g2632011] [LN:BSAJ2571] [AC:AJ002571] [PN:YkdA] [GN:ykdA] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis 168 56 kb DNA fragment between xlyA and ykoR.] [NT:putative serine protease, heat-shock inducible;] [LE:10063] [RE:11412] [DI:complement] >gp: [GI:e1183310:g2633644] [LN:BSUB0007] [AC:Z99110:AL009126] [PN:serine protease Do (heat-shock protein)] [GN:htrA] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 7 of 21): from 1194391 to 1411140.] [NT:alternate gene name: ykdA] [LE:163012] [RE:164361] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000993\_26567062\_c1\_642

2255 6027 792 263 428 3.3e-40

Description

pir: [LN:A69996] [AC:A69996] [PN:hypothetical protein ytmA] [GN:ytmA] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1185931:g2635542] [LN:BSUB0016] [AC:Z99119:AL009126] [GN:ytmA] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 16 of 21): from 2997771 to 3213410.] [LE:132757] [RE:133530] [DI:complement] >gp: [GI:g2293162] [LN:AF008220] [AC:AF008220] [PN:putative peptidase] [GN:ytmA] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis rrnB-dnaB genomic region.] [LE:46897] [RE:47670] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000993\_26596062\_f3\_484

2256 6028 1284 427 1198 8.3e-122

Description

gp: [GI:g2293312] [LN:AF008220] [AC:AF008220] [PN:YtfP] [GN:ytfP] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis rrnB-dnaB genomic region.] [NT:similarity to hypothetical protein f400 from E.] [LE:102487] [RE:103704] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000993\_2741536\_c2\_805

2257 6029 162 53

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000993\_2757633\_c2\_765

2258 6030 1494 497 1275 1.9e-164

Description

sp: [LN:MENE\_STAAU] [AC:Q53634] [GN:MENE] [OR:STAPHYLOCOCCUS AUREUS] [EC:6.2.1.26] [DE:(O-SUCCINYLBENZOATE-COA SYNTHASE)] [SP:Q53634] [DB:swissprot] >gp: [GI:g1255259] [LN:SAU51132] [AC:U51132] [PN:o-succinylbenzoic acid (OSB) CoA ligase] [GN:mene] [FN:converts OSB to OSB-CoA in menaquinone] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:Staphylococcus aureus o-succinylbenzoic acid CoA ligase (mene), and o-succinylbenzoic acid synthetase (menc) genes, complete cds.] [LE:491] [RE:1969] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000993\_2869676\_f2\_338

2259 6031 123 40

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000993_2923202_c1_699	2260	6032	1473	490	1202	3.1e-122

Description

gp: [GI:g1732197] [LN:VFU65014] [AC:U65014] [PN:PTS permease for N-acetylglucosamine and] [GN:nagE] [OR:Vibrio furnissii] [DB:genpept-bct2] [DE:Vibrio furnissii PTS permease for N-acetylglucosamine and glucose(nagE) gene, complete cds.] [NT:PTS enzyme IINag] [LE:115] [RE:1605] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503000993_29562552_f3_555	2261	6033	276	91	281	1.2e-24
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Description

pir: [LN:H69993] [AC:H69993] [PN:hypothetical protein ytjA] [GN:ytjA] [CL:conserved hypothetical protein HI1000] [OR:Bacillus subtilis] [DB:pir2]  
 >gp: [GI:e1185941:g2635552] [LN:BSUB0016] [AC:Z99119:AL009126] [GN:ytjA] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.] [LE:139407] [RE:139634] [DI:direct]  
 >gp: [GI:g2293294] [LN:AF008220] [AC:AF008220] [PN:YtjA] [GN:ytjA] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis rrnB-dnaB genomic region.] [NT:similar to hypothetical 9.3 kD protein from P.] [LE:40793] [RE:41020] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503000993_30079651_f1_66	2262	6034	1620	539	1135	4.0e-115
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Description

sp: [LN:SERA\_BACSU] [AC:P35136:O32011] [GN:SERA] [OR:BACILLUS SUBTILIS] [EC:1.1.1.95] [DE:D-3-PHOSPHOGLYCERATE DEHYDROGENASE, (PGDH)] [SP:P35136:O32011] [DB:swissprot]  
 >pir: [LN:C69705] [AC:C69705:S45534] [PN:phosphoglycerate dehydrogenase, serA] [GN:serA] [CL:Bacillus phosphoglycerate dehydrogenase] [OR:Bacillus subtilis] [EC:1.1.1.95] [DB:pir2] >gp: [GI:e1185576:g2634742] [LN:BSUB0013] [AC:Z99116:AL009126] [PN:phosphoglycerate dehydrogenase] [GN:serA] [FN:serine biosynthesis] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:1.1.1.95] [DE:Bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.] [SP:P35136] [LE:15060] [RE:16637] [DI:direct] >gp: [GI:g1146196] [LN:BACSER] [AC:L47648] [PN:phosphoglycerate dehydrogenase] [GN:serA] [FN:serine biosynthesis] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis phosphoglycerate dehydrogenase (serA), ypaA, ferredoxin (fer), ypbB, recS, ypbD, ypbE, ypbF, ypbG, ypbH, glutamate dehydrogenase (ypcA), ypdA, ypdB, ypdC, spore cortex lytic enzyme (sleB), ypeB, ypfA, ypfB, cytidine monophosphate kinase (cmk), ypfD, ypgA, yphA, yphB, yphC, NAD<sup>+</sup> dependent glycerol-3-phosphate dehydrogenase (glyc), yphE and yphF genes, complete cds.] [LE:40] [RE:1617] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503000993_30084402_f3_446	2263	6035	1188	395	716	1.0e-70
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Description

sp: [LN:DHSS\_SYNPI] [AC:P14776] [OR:SYNECHOCOCCUS SP] [SR:PCC 6716,] [EC:1.12.-.-] [DE:SUBUNIT] [SP:P14776] [DB:swissprot] >pir: [LN:HQYCSS] [AC:S06919] [PN:soluble hydrogenase, small chain] [CL:serine--pyruvate aminotransferase] [OR:Synechococcus sp.] [EC:1.12.-.-] [DB:pir1] >gp: [GI:g48054] [LN:SYNSOLHY] [AC:X16658] [OR:Synechococcus sp.] [SR:Synechococcus sp] [DB:genpept-bct1] [DE:Synechococcus DNA for the small subunit of soluble hydrogenase.] [NT:small subunit of soluble hydrogenase (AA 1-384)] [SP:P14776] [LE:226] [RE:1380] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000993_30114637_c3_847	2264	6036	1167	388	1177	1.4e-119

Description

pir:[LN:E69820] [AC:E69820] [PN:conserved hypothetical protein yhbA] [GN:yhbA] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1182880:g2633214] [LN:BSUB0005] [AC:Z99108:AL009126] [GN:yhbA] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 5 of 21): from 802821 to 1011250.] [NT:alternate gene name: ygaP; similar to hypothetical] [LE:164477] [RE:165784] [DI:direct] >gp:[GI:e308636:g1903044] [LN:BSZ93102] [AC:Z93102] [PN:hypothetical 48.5 kd protein] [GN:ygaP] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B. subtilis yga[L,M,N,O,P,Q,R,S,T], yzdB and yze[A,C] genes.] [LE:6803] [RE:8110] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000993_30274187_f3_522	2265	6037	969	322	1317	2.0e-134

Description

pir:[LN:D69999] [AC:D69999] [PN:conserved hypothetical protein ytqA] [GN:ytqA] [CL:Methanococcus jannaschii conserved hypothetical protein MJ0486] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1185921:g2635532] [LN:BSUB0016] [AC:Z99119:AL009126] [GN:ytqA] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 16 of 21): from 2997771 to 3213410.] [NT:similar to hypothetical proteins] [LE:121310] [RE:122278] [DI:direct] >gp:[GI:g2293302] [LN:AF008220] [AC:AF008220] [PN:YtqA] [GN:ytqA] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis rrnB-dnaB genomic region.] [NT:similarity to biotine synthase from B.sphaericus] [LE:58149] [RE:59117] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000993_30508255_c3_912	2266	6038	1416	471	1011	5.5e-102

Description

pir:[LN:S43914] [AC:S43914] [PN:hypothetical protein 1] [CL:peptidase V] [OR:Bacillus stearothermophilus] [DB:pir2] >gp:[GI:g436965] [LN:BACMALA] [AC:L13418] [OR:Bacillus stearothermophilus] [SR:Bacillus stearothermophilus (library: ATCC 7953) DNA] [DB:genpept-bct1] [DE:Bacillus stearothermophilus maltose permease (malA) gene, completecds.] [LE:24] [RE:1376] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000993_31256568_c2_817	2267	6039	201	66	114	6.2e-07

Description

pir:[LN:F71011] [AC:F71011] [PN:hypothetical protein PH1388] [GN:PH1388] [OR:Pyrococcus horikoshii] [DB:pir2] >gp:[GI:d1031437:g3257811] [LN:AP000006] [AC:AP000006:AB005215:AB009510:AB009511:AB009512:AB009513:AB009514] [PN:119aa long hypothetical protein] [GN:PH1388] [OR:Pyrococcus horikoshii] [SR:Pyrococcus horikoshii (strain:OT3) DNA, clone:Pyrococcus horikoshi] [DB:genpept-bct1] [DE:Pyrococcus horikoshii OT3 genomic DNA, 1166001-1485000 nt. position(6/7).] [LE:86760] [RE:87119] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000993_3140917_c3_954	2268	6040	189	62		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000993_31539156_c3_874	2269	6041	204	67		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000993_3158502_c2_792	2270	6042	225	74	122	2.7e-07

Description

pir: [LN:A69997] [AC:A69997] [PN:hypothetical protein ytmP] [GN:ytmP] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1185865:g2635476] [LN:BSUB0016] [AC:Z99119:AL009126] [GN:ytmP] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 16 of 21): from 2997771 to 3213410.] [LE:61986] [RE:62795] [DI:complement] >gp: [GI:g2293206] [LN:AF008220] [AC:AF008220] [PN:YtmP] [GN:ytmP] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis rrnB-dnaB genomic region.] [LE:117631] [RE:118440] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000993_33209677_c2_831	2271	6043	972	323	764	8.2e-76

Description

pir: [LN:F69999] [AC:F69999] [PN:conserved hypothetical protein ytqI] [GN:ytqI] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1184174:g2635390] [LN:BSUB0015] [AC:Z99118:AL009126] [GN:ytqI] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 15 of 21): from 2795131 to 3013540.] [NT:similar to hypothetical proteins] [LE:199851] [RE:200792] [DI:complement] >gp: [GI:g2293259] [LN:AF008220] [AC:AF008220] [PN:YtqI] [GN:ytqI] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis rrnB-dnaB genomic region.] [NT:similarity to MGPA protein from M.genitalium] [LE:182275] [RE:183216] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000993_33287515_f1_122	2272	6044	330	109	89	0.0022

Description

gp: [GI:g4091929] [LN:AF069752] [AC:AF069752] [PN:C5,6 desaturase] [GN:ERG3] [OR:Candida albicans] [DB:genpept-pln2] [DE:Candida albicans C5,6 desaturase (ERG3) gene, complete cds.] [LE:387] [RE:1547] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000993_33292165_f1_155	2273	6045	156	51		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000993_33317002_f1_114	2274	6046	123	40		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000993_33360312_f1_74	2275	6047	420	139	295	1.6e-25

Description

gp: [GI:e1284114:g2982646] [LN:SPAJ2293] [AC:AJ002293] [PN:penicillin-binding protein 1b] [GN:pbp1b] [OR:Streptococcus pneumoniae] [DB:genpept-bct1] [DE:Streptococcus pneumoniae pbp1b gene, partial, beta-lactamresistant.] [LE:<1] [RE:>1600] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000993_33647577_c2_740	2276	6048	1386	461	1586	6.4e-163

Description

gp: [GI:e1249821:g2832825] [LN:BS43KBDNA] [AC:AJ223978] [PN:fumarase protein, CitG] [GN:citG] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis 42.7kB DNA fragment from yvsA to yvqA.] [LE:37816] [RE:39204] [DI:direct]  
 >gp: [GI:e1184383:g2635801] [LN:BSUB0017] [AC:Z99120:AL009126] [PN:fumarate hydratase] [GN:citG] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:4.2.1.2] [DE:Bacillus subtilis complete genome (section 17 of 21): from 3197001 to 3414420.] [LE:191083] [RE:192471] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000993_33650137_c2_794	2277	6049	207	68	177	1.3e-13

Description

pir: [LN:A69999] [AC:A69999] [PN:phenylalanyl-tRNA synthetase (beta subunit) homolog ytpR] [GN:ytpR] [CL:Mycoplasma genitalium hypothetical protein MG449] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1185855:g2635466] [LN:BSUB0016] [AC:Z99119:AL009126] [GN:ytpR] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 16 of 21): from 2997771 to 3213410.] [NT:similar to phenylalanyl-tRNA synthetase (beta) [LE:54055] [RE:54660] [DI:complement]  
 >gp: [GI:g2293213] [LN:AF008220] [AC:AF008220] [PN:YtpR] [GN:ytpR] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis rrnB-dnaB genomic region.] [NT:similarity to phenylalanine tRNA ligase of E. coli] [LE:125766] [RE:126371] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000993_3365887_c2_791	2278	6050	630	209	501	6.0e-48

Description

pir: [LN:A69997] [AC:A69997] [PN:hypothetical protein ytmP] [GN:ytmP] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1185865:g2635476] [LN:BSUB0016] [AC:Z99119:AL009126] [GN:ytmP] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 16 of 21): from 2997771 to 3213410.] [LE:61986] [RE:62795] [DI:complement] >gp: [GI:g2293206] [LN:AF008220] [AC:AF008220] [PN:YtmP] [GN:ytmP] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis rrnB-dnaB genomic region.] [LE:117631] [RE:118440] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000993_33792687_c1_629	2279	6051	129	42		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000993_33831512_f2_373	2280	6052	234	77	82	0.0093

Description

gp: [GI:e1346461:g3876981] [LN:CEF40D4] [AC:Z81536] [GN:F40D4.10] [OR:Caenorhabditis elegans] [DB:genpept-inv1] [DE:Caenorhabditis elegans cosmid F40D4, complete sequence.] [LE:20486:20882:21041:21585] [RE:20830:20997:21200:21746] [DI:directJoin]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000993_33985077_c1_720	2281	6053	1230	409	1529	7.0e-157

Description

pir: [LN:C70001] [AC:C70001] [PN:malate dehydrogenase homolog ytsJ] [GN:ytsJ] [CL:malate dehydrogenase (oxaloacetate-decarboxylating)] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1184171:g2635387] [LN:BSUB0015] [AC:Z99118:AL009126] [GN:ytsJ] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.] [NT:similar to malate dehydrogenase] [LE:193843] [RE:195075] [DI:complement] >gp: [GI:g2293261] [LN:AF008220] [AC:AF008220] [PN:YtsJ] [GN:ytsJ] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis rrnB-dnaB genomic region.] [NT:similarity to malate dehydrogenase (NADP+) from] [LE:187992] [RE:189224] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000993_34177127_c1_721	2282	6054	1806	601	1853	3.3e-191

Description

sp: [LN:KPYK\_BACLI] [AC:P51181] [GN:PYK] [OR:BACILLUS LICHENIFORMIS] [EC:2.7.1.40] [DE:PYRUVATE KINASE, (PK)] [SP:P51181] [DB:swissprot] >pir: [LN:JC4220] [AC:JC4220] [PN:pyruvate kinase, :ATP:pyruvate 2-O-phosphotransferase] [CL:pyruvate kinase] [OR:Bacillus licheniformis] [EC:2.7.1.40] [DB:pir2] >gp: [GI:d1007299:g1041099] [LN:BACPYK2] [AC:D31955] [PN:Pyruvate Kinase] [OR:Bacillus licheniformis] [SR:Bacillus licheniformis DNA] [DB:genpept-bct1] [DE:Bacillus licheniformis gene for pyruvate kinase, complete cds.] [LE:132] [RE:1889] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000993_34178128_c3_888	2283	6055	216	71		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000993_34181551_c2_841	2284	6056	924	307	618	2.4e-60

Description

sp: [LN:DNAI\_BACSU] [AC:P06567] [GN:DNAI] [OR:BACILLUS SUBTILIS] [DE:PRIMOSOMAL PROTEIN DNAI] [SP:P06567] [DB:swissprot] >pir: [LN:IQBS44] [AC:B24720:C26580:F69617] [PN:primosome component (helicase loader) dnaI:dnaA protein homolog, 44K:hypothetical protein Y (dnaB 3' region)] [GN:dnaI] [CL:44K dnaA protein homolog] [OR:Bacillus subtilis] [DB:pir1] >gp: [GI:g39881] [LN:BSDNAB] [AC:X04963] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis dnaB gene for initiation of chromosomal replication.] [NT:ORF 311 (AA 1-311)] [SP:P06567] [LE:1843] [RE:2778] [DI:direct] >gp: [GI:e1184147:g2635363] [LN:BSUB0015] [AC:Z99118:AL009126] [PN:helicase loader] [GN:dnaI] [FN:DNA synthesis] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 15 of 21): from 2795131 to 3013540.] [NT:alternate gene name: ytxA, dnaY] [SP:P06567] [LE:167129] [RE:168064] [DI:complement] >gp: [GI:e1165286:g1769996] [LN:BSZ75208] [AC:Z75208] [PN:replication protein] [GN:dnaI] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis genomic sequence 89009bp.] [NT:DNA synthesis; putative primosome component] [SP:P06567] [LE:1843] [RE:2778] [DI:direct] >gp: [GI:g2293281] [LN:AF008220] [AC:AF008220] [PN:DnaI] [GN:dnaI] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis rrnB-dnaB genomic region.] [LE:215003] [RE:215938] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000993_34199077_c3_883	2285	6057	1017	338	864	2.1e-86

Description

gp: [GI:g1255260] [LN:SAU51132] [AC:U51132] [PN:o-succinylbenzoic acid (OSB) synthetase] [GN:menc] [FN:converts SHCHC to OSB in menaquinone] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:Staphylococcus aureus o-succinylbenzoic acid CoA ligase (mene), and o-succinylbenzoic acid synthetase (menc) genes, complete cds.] [LE:1974] [RE:2975] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000993_34272752_c3_862	2286	6058	963	320	1413	1.4e-144

Description

gp: [GI:g710422] [LN:SAU21636] [AC:U21636] [PN:cmp-binding-factor 1] [GN:cbf1] [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus cmp-binding-factor 1 (cbf1) and ORF X genes, complete cds.] [LE:1155] [RE:2096] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000993_34415925_c3_914	2287	6059	654	217	540	4.5e-52

Description

pir: [LN:B69997] [AC:B69997] [PN:conserved hypothetical protein ytmQ] [GN:ytmQ] [CL:hypothetical protein HI0340] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1185863:g2635474] [LN:BSUB0016] [AC:Z99119:AL009126] [GN:ytmQ] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 16 of 21): from 2997771 to 3213410.] [NT:similar to hypothetical proteins] [LE:60859] [RE:61500] [DI:complement] >gp: [GI:g2293207] [LN:AF008220] [AC:AF008220] [PN:YtmQ] [GN:ytmQ] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis rrnB-dnaB genomic region.] [NT:similar to hypothetical protein HI0340 from H.] [LE:118926] [RE:119567] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000993_34429838_c3_884	2288	6060	483	160	261	1.6e-22

Description

pir:[LN:E69994] [AC:E69994] [PN:hypothetical protein ytkD] [GN:ytkD] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1185936:g2635547] [LN:BSUB0016] [AC:Z99119:AL009126] [GN:ytkD] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 16 of 21): from 2997771 to 3213410.] [LE:136293] [RE:136769] [DI:complement] >gp:[GI:g2293161] [LN:AF008220] [AC:AF008220] [PN:YtkD] [GN:ytkD] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis rrnB-dnaB genomic region.] [LE:43658] [RE:44134] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000993_34610925_f3_445	2289	6061	462	153	274	6.9e-24

Description

pir:[LN:F69883] [AC:F69883] [PN:conserved hypothetical protein ymaD] [GN:ymaD] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1183387:g2634112] [LN:BSUB0010] [AC:Z99113:AL009126] [GN:ymaD] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 10 of 21): from 1781201 to 2014980.] [NT:similar to hypothetical proteins] [LE:82267] [RE:82719] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000993_34617017_c3_869	2290	6062	759	252	773	9.1e-77

Description

sp:[LN:ECSA\_BACSU] [AC:P55339] [GN:ECSA:PRST] [OR:BACILLUS SUBTILIS] [DE:ABC-TYPE TRANSPORTER ATP-BINDING PROTEIN ECSA] [SP:P55339] [DB:swissprot] >pir:[LN:F69619] [AC:F69619] [PN:ABC transporter (ATP-binding protein) ecsA] [GN:ecsA] [CL:ATP-binding cassette homology] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e183449:g1177253] [LN:BSECSABCG] [AC:X87807] [PN:putative ATP-binding protein of ABC-type] [GN:ecsA] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B. subtilis ecsA, ecsB, and ecsC genes.] [SP:P55339] [LE:248] [RE:991] [DI:direct] >gp:[GI:e1183006:g2633340] [LN:BSUB0006] [AC:Z99109:AL009126] [PN:ABC transporter (ATP-binding protein)] [GN:ecsA] [FN:regulates both components of the protein] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 6 of 21): from 999501 to 1209940.] [NT:alternate gene name: prst, ecs-26, yhaD] [SP:P55339] [LE:77413] [RE:78156] [DI:direct] >gp:[GI:e324952:g2226115] [LN:BSY14077] [AC:Y14077] [PN:Hypothetical protein] [GN:yhaD] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis 10.6 Kb chromosomal DNA: glyB-prsA region.] [NT:Identified as ecsA. Similar to many ATP binding ABC] [SP:P55339] [LE:2757] [RE:3500] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000993_35360932_c3_944	2291	6063	1278	425	1493	4.6e-153

Description

sp: [LN:ACKA\_BACSU] [AC:P37877] [GN:ACKA] [OR:BACILLUS SUBTILIS] [EC:2.7.2.1] [DE:ACETATE KINASE, (ACETOKINASE)] [SP:P37877] [DB:swissprot] >pir: [LN:B49935] [AC:B49935:C69581] [PN:acetate kinase, ackA] [GN:ackA] [CL:acetate kinase] [OR:Bacillus subtilis] [EC:2.7.2.1] [DB:pir2] >gp: [GI:e1185820:g2635431] [LN:BSUB0016] [AC:Z99119:AL009126] [PN:acetate kinase] [GN:ackA] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:2.7.2.1] [DE:Bacillus subtilis complete genome (section 16 of 21): from 2997771 to 3213410.] [SP:P37877] [LE:16413] [RE:17600] [DI:complement] >gp: [GI:g2293240] [LN:AF008220] [AC:AF008220] [PN:acetate kinase] [GN:ackA] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis rrnB-dnaB genomic region.] [LE:162827] [RE:164014] [DI:direct] >gp: [GI:g405134] [LN:BACACKA] [AC:L17320] [PN:acetate kinase] [GN:ackA] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain W168) DNA] [DB:genpept-bct2] [DE:Bacillus subtilis acetate kinase (ackA) gene, complete cds.] [LE:698] [RE:1885] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000993_36152191_c3_863	2292	6064	126	41		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000993_36541078_c1_647	2293	6065	171	56		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000993_3906642_c1_632	2294	6066	600	199	244	1.0e-20

Description

pir: [LN:H69778] [AC:H69778] [PN:hypothetical protein ydeN] [GN:ydeN] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:d1020114:g1881334] [LN:AB001488] [AC:AB001488] [GN:ydeN] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:168) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis genome sequence, 148 kb sequence of the region between 35 and 47 degree.] [NT:FUNCTION UNKNOWN.] [LE:106671] [RE:107243] [DI:complement] >gp: [GI:e1182492:g2632826] [LN:BSUB0003] [AC:Z99106:AL009126] [GN:ydeN] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 3 of 21): from 402751 to 611850.] [LE:170416] [RE:170988] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000993_3944015_c1_608	2295	6067	540	179	331	6.2e-30

Description

pir: [LN:S68867] [AC:S68867:S54422] [PN:probable transport protein arpJ:ABC transporter arpJ] [OR:Listeria monocytogenes] [DB:pir2]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000993_4073892_c1_631	2296	6068	1458	485	1083	1.3e-109

Description

sp: [LN:PPOX\_BACSU] [AC:P32397] [GN:HEMY:HEMG] [OR:BACILLUS SUBTILIS] [EC:1.3.3.4] [DE:PROTOPORPHYRINOGEN OXIDASE, (PPO)] [SP:P32397] [DB:swissprot] >pir:[LN:D47045] [AC:D47045:D69640] [PN:coproporphyrinogen III oxidase / protoporphyrinogen IX oxidase hemY] [GN:hemY] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:g143045] [LN:BACHEMEHY] [AC:M97208] [GN:hemY] [FN:involved in a late step of protoheme IX] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain W168) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis penicillin binding protein 1A (ponA) gene; uroporphyrinogen decarboxylase (hemE) gene; ferrochelatase (hemH) gene complete cds, (hemY) gene, complete cds; ORFA, complete cds; ORFB 5' end.] [LE:3985] [RE:5397] [DI:direct] >gp:[GI:e1183016:g2633350] [LN:BSUB0006] [AC:Z99109:AL009126] [PN:protoporphyrinogen IX and coproporphyrinogen III] [GN:hemY] [FN:late steps of protoheme IX synthesis (porphyrin)] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:1.3.3.4] [DE:Bacillus subtilis complete genome (section 6 of 21): from 999501 to 1209940.] [NT:alternate gene name: hemG] [SP:P32397] [LE:88170] [RE:89582] [DI:direct] >gp:[GI:e325009:g2226232] [LN:BSY14083] [AC:Y14083] [PN:Protoporphyrinogen IX oxidase] [GN:hemY] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis chromosomal DNA, region 76-78 degrees: between glyB-aprE.] [NT:see Swiss Prot P32397; HEMG\_BACSU.] [SP:P32397] [LE:8029] [RE:9441] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000993_4110882_f3_473	2297	6069	351	116	90	0.00022

Description

pir: [LN:D70004] [AC:D70004] [PN:hypothetical protein ytzB] [GN:ytzB] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1185860:g2635471] [LN:BSUB0016] [AC:Z99119:AL009126] [GN:ytzB] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 16 of 21): from 2997771 to 3213410.] [LE:57791] [RE:58108] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000993_4173427_c2_742	2298	6070	474	157	82	0.0020

Description

pir: [LN:A64334] [AC:A64334] [PN:hypothetical protein MJ0272] [OR:Methanococcus jannaschii] [DB:pir2] [MP:FOR257413-257652] >gp:[GI:g1590997] [LN:U67482] [AC:U67482:L77117] [PN:repressor protein, putative (yorfE)] [GN:MJ0272] [OR:Methanococcus jannaschii] [DB:genpept-bct2] [DE:Methanococcus jannaschii section 24 of 150 of the complete genome.] [NT:similar to GP:1536960 percent identity: 40.32;] [LE:5633] [RE:5872] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000993_4183428_c3_921	2299	6071	1329	442	1966	3.5e-203

Description

sp: [LN:MURC\_STAAU] [AC:O31211] [GN:MURC] [OR:STAPHYLOCOCCUS AUREUS] [EC:6.3.2.8] [DE:ACETYL MURANOYL-L-ALANINE SYNTHETASE] [SP:O31211] [DB:swissprot] >gp:[GI:g2642659] [LN:AF034076] [AC:AF034076] [PN:UDP-N-acetylmuramoyl-L-alanine synthetase] [GN:murC] [FN:cell wall biosynthesis] [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus UDP-N-acetylmuramoyl-L-alanine synthetase (murC) gene, complete cds.] [NT:MurC; UDP-N-acetylmuramate-alanine ligase] [LE:1] [RE:1314] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000993_4296950_c2_764	2300	6072	198	65		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000993_4299175_c1_637	2301	6073	240	79	102	0.00012

Description

pir:[LN:T00158] [AC:T00158] [PN:amidase,] [OR:Staphylococcus aureus phage phi PVL] [EC:3.5.-.-] [DB:pir3] >gp:[GI:d1032859:g3341932] [LN:AB009866] [AC:AB009866] [PN:amidase (peptidoglycan hydrolase)] [OR:bacteriophage phi PVL] [SR:bacteriophage phi PVL (specific\_host:Staphylococcus aureus ATC) [DB:genpept-phg] [DE:Bacteriophage phi PVL proviral DNA, complete sequence.] [NT:orf 25] [LE:20199] [RE:21653] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000993_4345967_f2_357	2302	6074	441	146	368	7.5e-34

Description

sp:[LN:HIT\_BACSU] [AC:007513] [GN: HIT] [OR:BACILLUS SUBTILIS] [DE:HIT PROTEIN] [SP:007513] [DB:swissprot] >pir:[LN:A69642] [AC:A69642] [PN:cell-cycle regulation histidine triad (HIT) protein] [GN:hit] [CL:protein kinase C inhibitor:histidine triad homology] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1183005:g2633339] [LN:BSUB0006] [AC:Z99109:AL009126] [PN:Hit-like protein] [GN:hit] [FN:cell-cycle regulation (inhibition of cell] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 6 of 21): from 999501 to 1209940.] [NT:alternate gene name: yhaE] [SP:007513] [LE:76488] [RE:76925] [DI:complement] >gp:[GI:e325178:g2226116] [LN:BSY14077] [AC:Y14077] [PN:Hypothetical protein] [GN:yhaE] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis 10.6 Kb chromosomal DNA: glyB-prsA region.] [NT:Similarity to the Hit family of proteins] [SP:007513] [LE:3988] [RE:4425] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000993_4453537_c3_937	2303	6075	159	52		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000993_4459380_c1_712	2304	6076	207	68		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000993_4502308_c2_812	2305	6077	636	211	502	4.7e-48

Description

pir:[LN:E69826] [AC:E69826] [PN:1-acylglycerol-3-phosphate O-acyltransferase homolog yhdO] [GN:yhdO] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1182955:g2633289] [LN:BSUB0006] [AC:Z99109:AL009126] [GN:yhdO] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 6 of 21): from 999501 to 1209940.] [NT:similar to 1-acylglycerol-3-phosphate] [LE:31375] [RE:31974] [DI:direct] >gp:[GI:e325031:g2226210] [LN:BSY14082] [AC:Y14082] [PN:hypothetical protein] [GN:yhdO] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis chromosomal DNA, region 72 to 75 degrees: spoVRto sspB.] [NT:Similarity to a hypothetical protein from] [LE:18023] [RE:18622] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000993_4511283_c3_859	2306	6078	153	50		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000993_4568761_c1_630	2307	6079	1116	371	1257	4.7e-128

Description

sp: [LN:DCUP\_BACSU] [AC:P32395] [GN:HEME] [OR:BACILLUS SUBTILIS] [EC:4.1.1.37] [DE:UROPORPHYRINOGEN DECARBOXYLASE, (UPD)] [SP:P32395] [DB:swissprot] >pir: [LN:B47045] [AC:B47045:G69639] [PN:uroporphyrinogen decarboxylase, hemE:uroporphyrinogen III decarboxylase hemE] [GN:hemE] [CL:uroporphyrinogen decarboxylase] [OR:Bacillus subtilis] [EC:4.1.1.37] [DB:pir2] >gp: [GI:g143043] [LN:BACHEMEHY] [AC:M97208] [PN:uroporphyrinogen decarboxylase] [GN:hemE] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain W168) DNA] [DB:genpept-bct1] [EC:4.1.1.37] [DE:Bacillus subtilis penicillin binding protein 1A (ponA) gene;uroporphyrinogen decarboxylase (hemE) gene; ferrochelatase (hemH) gene complete cds, (hemY) gene, complete cds; ORFA, complete cds;ORFB 5' end.] [LE:1905] [RE:2966] [DI:direct] >gp: [GI:e1183014:g2633348] [LN:BSUB0006] [AC:Z99109:AL009126] [PN:uroporphyrinogen III decarboxylase] [GN:hemE] [FN:porphyrin biosynthesis] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:4.1.1.37] [DE:Bacillus subtilis complete genome (section 6 of 21): from 999501 to 1209940.] [SP:P32395] [LE:86090] [RE:87151] [DI:direct] >gp: [GI:e325194:g2226230] [LN:BSY14083] [AC:Y14083] [PN:Uroporphyrinogen III decarboxylase] [GN:hemE] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:4.1.1.37] [DE:Bacillus subtilis chromosomal DNA, region 76-78 degrees: between B-aprE.] [NT:see Swiss Prot P32395; DCUP\_BACSU.] [SP:P32395] [LE:5949] [RE:7010] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000993_4579675_f3_569	2308	6080	129	42		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000993_4693800_f2_225	2309	6081	570	189	191	4.3e-15

Description

pir: [LN:A69220] [AC:A69220] [PN:conserved hypothetical protein MTH898] [GN:MTH898] [CL:Escherichia coli ybdQ protein] [OR:Methanobacterium thermoautotrophicum] [DB:pir2] >gp: [GI:g2621993] [LN:AE000865] [AC:AE000865:AE000666] [PN:conserved protein] [GN:MTH898] [OR:Methanobacterium thermoautotrophicum] [DB:genpept-bct1] [DE:Methanobacterium thermoautotrophicum from bases 808939 to 820180 (section 71 of 148) of the complete genome.] [NT:Function Code:14.01 - Unknown, Conserved protein;] [LE:6700] [RE:7149] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000993_4697318_c3_919	2310	6082	867	288	671	5.8e-66

Description

pir: [LN:H69998] [AC:H69998] [PN:hypothetical protein ytpQ] [GN:ytpQ] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1185856:g2635467] [LN:BSUB0016] [AC:Z99119:AL009126] [GN:ytpQ] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 16 of 21): from 2997771 to 3213410.] [LE:54676] [RE:55485] [DI:complement] >gp: [GI:g2293212] [LN:AF008220] [AC:AF008220] [PN:YtpQ] [GN:ytpQ] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis rrnB-dnaB genomic region.] [LE:124941] [RE:125750] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000993_472538_c1_707	2311	6083	144	47		

Description

NO-HIT

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000993_4776702_c1_669	2312	6084	312	103	164	3.1e-12

Description

sp: [LN:YRKF\_BACSU] [AC:P54433] [GN:YRKF] [OR:BACILLUS SUBTILIS] [DE:HYPOTHETICAL 20.7 KD PROTEIN IN BLTR-SPOIIIC INTERGENIC REGION] [SP:P54433] [DB:swissprot]  
>pir: [LN:D69976] [AC:D69976] [PN:conserved hypothetical protein yrkf] [GN:yrkf] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:d1013040:g1303705] [LN:BACJH642] [AC:D84432:D82370] [PN:YrkF] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:JH642(trpC2 PheA1)) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis DNA, 283 Kb region containing skin element.] [LE:6477] [RE:7034] [DI:direct]  
>gp: [GI:e1183882:g2635098] [LN:BSUB0014] [AC:Z99117:AL009126] [GN:yrkf] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 14 of 21): from 2599451 to 2812870.] [NT:similar to hypothetical proteins from B. subtilis] [SP:P54433] [LE:112396] [RE:112953] [DI:complement]

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000993_4876300_c2_806	2313	6085	1695	564	1845	2.3e-190

Description

sp: [LN:FTHS\_STRMU] [AC:Q59925:Q59926] [GN:FHS] [OR:STREPTOCOCCUS MUTANS] [EC:6.3.4.3] [DE:SYNTHETASE] (FHS) (FTHFS) [SP:Q59925:Q59926] [DB:swissprot] >gp: [GI:g1103865] [LN:SMU39612] [AC:U39612] [PN:formyl-tetrahydrofolate synthetase] [GN:fhs] [FN:enzyme involved in the formation of] [OR:Streptococcus mutans] [DB:genpept-bct1] [EC:6.3.4.3] [DE:Streptococcus mutans formyl-tetrahydrofolate synthetase (fhs) gene, complete cds.] [NT:formyl-tetrahydrofolate ligase; ATP-dependant] [LE:115] [RE:1785] [DI:direct]

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000993_4876718_c1_617	2314	6086	1143	380	810	1.1e-80

Description

pir: [LN:E69824] [AC:E69824] [PN:two-component sensor histidine kinase homolog yhcY] [GN:yhcY] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1182921:g2633255] [LN:BSUB0005] [AC:Z99108:AL009126] [GN:yhcY] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 5 of 21): from 802821 to 1011250.] [NT:similar to two-component sensor histidine kinase] [LE:205305] [RE:206444] [DI:direct] >gp: [GI:e1182933:g2633267] [LN:BSUB0006] [AC:Z99109:AL009126] [GN:yhcY] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 6 of 21): from 999501 to 1209940.] [NT:similar to two-component sensor histidine kinase] [LE:8625] [RE:9764] [DI:direct] >gp: [GI:e1191876:g2226140] [LN:BSY14079] [AC:Y14079] [PN:hypothetical protein] [GN:yhcY] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis chromosomal DNA, region 75 degrees: glpPFKdoperon and downstream.] [NT:similarity to the sensory transduction kinase degS] [LE:8273] [RE:9412] [DI:direct]

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000993_4882963_f3_591	2315	6087	834	277	457	2.8e-43

Description

sp: [LN:YHCT\_BACSU] [AC:P54604] [GN:YHCT] [OR:BACILLUS SUBTILIS] [DE:HYPOTHETICAL 33.7 KD PROTEIN IN CSPB-GLPP INTERGENIC REGION] [SP:P54604] [DB:swissprot] >pir: [LN:H69823] [AC:H69823] [PN:conserved hypothetical protein yhct] [GN:yhct] [CL:conserved hypothetical protein HI0176] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e233879:g1239996] [LN:BS75DGREG] [AC:X96983] [PN:hypothetical protein] [GN:yhct] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B. subtilis chromosomal DNA (region 75 degrees: cspB upstream of glpPFKD operon).] [NT:Similarity to DRAP deaminase from Saccharomyces] [SP:P54604] [LE:16504] [RE:17412] [DI:complement] >gp: [GI:e1182910:g2633244] [LN:BSUB0005] [AC:Z99108:AL009126] [GN:yhct] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 5 of 21): from 802821 to 1011250.] [NT:similar to hypothetical proteins] [SP:P54604] [LE:192310] [RE:193218] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000993_4938877_c2_778	2316	6088	147	48		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000993_5081252_f2_327	2317	6089	360	119	199	6.1e-16

Description

pir: [LN:A70341] [AC:A70341] [PN:conserved hypothetical protein aq\_449] [GN:aq\_449] [CL:hypothetical protein MJ1523] [OR:Aquifex aeolicus] [DB:pir2] >gp: [GI:g2983116] [LN:AE000690] [AC:AE000690:AE000657] [PN:hypothetical protein] [GN:aq\_449] [OR:Aquifex aeolicus] [DB:genpept-bct2] [DE:Aquifex aeolicus section 22 of 109 of the complete genome.] [LE:10789] [RE:11163] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000993_5132078_c3_845	2318	6090	729	242	752	1.5e-74

Description

pir: [LN:H69334] [AC:H69334] [PN:glutamine transport protein glnQ] [GN:glnQ] [CL:inner membrane protein malK:ATP-binding cassette homology] [OR:Archaeoglobus fulgidus] [DB:pir2] >gp: [GI:g2649950] [LN:AE001058] [AC:AE001058:AE000782] [PN:glutamine ABC transporter, ATP-binding protein] [GN:AF0680] [OR:Archaeoglobus fulgidus] [DB:genpept-bct2] [DE:Archaeoglobus fulgidus section 49 of 172 of the complete genome.] [NT:similar to GB:M61017 SP:P27675 PID:142988 percent] [LE:10147] [RE:10875] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000993_5135265_c3_967	2319	6091	504	167	438	2.9e-41

Description

gp: [GI:g4982284] [LN:AE001810] [AC:AE001810:AE000512] [PN:conserved hypothetical protein] [GN:TM1707] [OR:Thermotoga maritima] [DB:genpept-bct2] [DE:Thermotoga maritima section 122 of 136 of the complete genome.] [NT:similar to GB:M15183 PID:468267 PID:2293279] [LE:13832] [RE:14302] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000993_5273425_c2_735	2320	6092	1053	350	473	5.6e-45

Description

gp: [GI:g4981111] [LN:AE001734] [AC:AE001734:AE000512] [PN:amino acid ABC transporter, permease protein] [GN:TM0592] [OR:Thermotoga maritima] [DB:genpept-bct2] [DE:Thermotoga maritima section 46 of 136 of the complete genome.] [NT:similar to GB:AE000782 percent identity: 72.86;] [LE:3214] [RE:3864] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000993_5355250_c1_696	2321	6093	1284	427	1343	3.6e-137

Description

sp: [LN:SYB\_BACST] [AC:P00952] [GN:TYRS] [OR:BACILLUS STEAROTHERMOPHILUS] [EC:6.1.1.1] [DE:TYROSYL-TRNA SYNTHETASE, (TYROSINE--TRNA LIGASE) (TYRRS)] [SP:P00952] [DB:swissprot] >pir: [LN:SYBSYF] [AC:A01179:I40506] [PN:tyrosine--tRNA ligase, :tyrosyl-tRNA synthetase] [CL:tyrosine--tRNA ligase] [OR:Bacillus stearothermophilus] [EC:6.1.1.1] [DB:pir1]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000993_551907_f3_559	2322	6094	708	235	183	3.0e-14

Description

gp: [GI:g2897104] [LN:AF020798] [AC:AF020798] [PN:putative host cell surface-exposed lipoprotein] [OR:Streptococcus thermophilus bacteriophage TP-J34] [DB:genpept-phg] [DE:Streptococcus thermophilus bacteriophage lysogeny module, integrasehomolog (int), putative host cell surface-exposed lipoprotein,putative metallo-proteinase, repressor, Cro-like regulatoryprotein, and P1-antirepressor homolog genes, complete cds.] [NT:orf142] [LE:3941] [RE:4369] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000993_572186_c1_692	2323	6095	1284	427	190	2.4e-11

Description

pir: [LN:I51116] [AC:I51116] [PN:NF-180] [OR:Petromyzon marinus] [SR:, sea lamprey] [DB:pir2] >gp: [GI:g632549] [LN:PMU19361] [AC:U19361] [PN:NF-180] [OR:Petromyzon marinus] [SR:sea lamprey] [DB:genpept-vrt] [DE:Petromyzon marinus neurofilament subunit NF-180 mRNA, complete cds.] [NT:180 kDa neurofilament subunit] [LE:122] [RE:3454] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000993_581382_f2_281	2324	6096	183	60	46	0.040

Description

sp: [LN:PA2A\_PSETE] [AC:P23026] [OR:PSEUDONAJA TEXTILIS] [SR:, EASTERN BROWN SNAKE] [EC:3.1.1.4] [DE:PHOSPHOLIPASE A2 HOMOLOG, TEXTILOTOXIN A CHAIN,] [SP:P23026] [DB:swissprot] >pir: [LN:S29651] [AC:S29651] [PN:textilotoxin chain A] [CL:phospholipase A2] [OR:Pseudonaja textilis] [SR:, eastern brown snake] [DB:pir2]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000993_5882753_c3_956	2325	6097	273	90		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000993_5911592_c3_887	2326	6098	924	307	89	0.0048

Description

gp: [GI:e1347496:g3877859] [LN:CEF58G6] [AC:Z68217] [GN:F58G6.1] [OR:Caenorhabditis elegans] [DB:genpept-inv1] [DE:Caenorhabditis elegans cosmid F58G6, complete sequence.] [NT:Similarity to Chicken amphiphysin (PIR Acc. No.)] [LE:4939:5597:5746] [RE:5253:5662:5844] [DI:complementJoin]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000993_6070392_c3_911	2327	6099	708	235	458	2.2e-43

Description

gp: [GI:g4980760] [LN:AE001708] [AC:AE001708:AE000512] [PN:16S pseudouridylate synthase] [GN:TM0264] [OR:Thermotoga maritima] [DB:genpept-bct2] [DE:Thermotoga maritima section 20 of 136 of the complete genome.] [NT:similar to SP:P33918 PID:405907 GB:U00096] [LE:17059] [RE:17778] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000993_6100150_c3_881	2328	6100	189	62		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000993_6125262_c2_840	2329	6101	192	63	71	0.022

Description

pir: [LN:S72295] [AC:S72295] [PN:ribosomal protein S8] [GN:rps8] [OR:plastid Plasmodium falciparum] [DB:pir2] >gp: [GI:e220199:g1171601] [LN:PFCOMPIRB] [AC:X95276] [GN:rps8] [OR:Plasmodium falciparum] [SR:malaria parasite P. falciparum] [DB:genpept-inv1] [DE:P. falciparum complete gene map of plastid-like DNA (IR-B).] [LE:5492] [RE:5878] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000993_6317_c1_687	2330	6102	411	136	267	3.8e-23

Description

pir: [LN:G69998] [AC:G69998] [PN:thioredoxin H1 homolog ytpP] [GN:ytpP] [CL:thioredoxin:thioredoxin homology] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1185857:g2635468] [LN:BSUB0016] [AC:Z99119:AL009126] [GN:ytpP] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 16 of 21): from 2997771 to 3213410.] [NT:similar to thioredoxin H1] [LE:55500] [RE:55823] [DI:complement] >gp: [GI:g2293211] [LN:AF008220] [AC:AF008220] [PN:putative thioredoxin] [GN:ytpP] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis rrnB-dnaB genomic region.] [LE:124603] [RE:124926] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000993_6689717_c3_849	2331	6103	615	204	72	0.0043

Description

gp: [GI:g4105715] [LN:AF050754] [AC:AF050754] [PN:glucose 6-phosphate isomerase] [GN:GPI1] [OR:Giardia intestinalis] [DB:genpept-inv2] [EC:5.3.1.10] [DE:Giardia intestinalis glucose 6-phosphate isomerase (GPI1) gene, complete cds.] [NT:aminating isomerase] [LE:432] [RE:1232] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000993_6828305_f3_438	2332	6104	132	43		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000993_6906300_c2_826	2333	6105	1014	337	519	7.5e-50

Description

sp:[LN:YTXK\_BACSU] [AC:P37876] [GN:YTXK] [OR:BACILLUS SUBTILIS] [DE:HYPOTHETICAL 37.4 KD PROTEIN IN ACKA-SSPA INTERGENIC REGION] [SP:P37876] [DB:swissprot] >pir:[LN:G70003] [AC:G70003:A49935] [PN:hypothetical protein ytxK:hypothetical protein (ackA 5' region)] [GN:ytxK] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1185821:g2635432] [LN:BSUB0016] [AC:Z99119:AL009126] [GN:ytxK] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.] [NT:alternate gene name: ythI] [SP:P37876] [LE:17948] [RE:18937] [DI:complement] >gp:[GI:g2293239] [LN:AF008220] [AC:AF008220] [PN:YtxK] [GN:ytxK] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis rrnB-dnaB genomic region.] [NT:similarity to modification metilase AccI] [LE:161490] [RE:162479] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000993_6929651_c3_858	2334	6106	366	121	289	1.8e-25

Description

pir:[LN:A69828] [AC:A69828] [PN:hypothetical protein yheA] [GN:yheA] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1182981:g2633315] [LN:BSUB0006] [AC:Z99109:AL009126] [GN:yheA] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 6 of 21): from 999501 to 1209940.] [LE:54726] [RE:55079] [DI:direct] >gp:[GI:e324964:g2226157] [LN:BSY14080] [AC:Y14080] [PN:hypothetical protein] [GN:yheA] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis chromosomal DNA, region 75 degrees: sspB upstreamof glyB.] [LE:6651] [RE:7004] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000993_7066588_c1_719	2335	6107	3204	1067	1849	5.1e-212

Description

sp:[LN:DP3A\_BACSU] [AC:O34623] [GN:DNAE] [OR:BACILLUS SUBTILIS] [EC:2.7.7.7] [DE:DNA POLYMERASE III, ALPHA CHAIN,] [SP:O34623] [DB:swissprot] >pir:[LN:D69617] [AC:D69617] [PN:DNA polymerase III (alpha subunit) dnaE] [GN:dnaE] [CL:DNA-directed DNA polymerase III alpha chain] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1184172:g2635388] [LN:BSUB0015] [AC:Z99118:AL009126] [PN:DNA polymerase III (alpha subunit)] [GN:dnaE] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.] [SP:O34623] [LE:195212] [RE:198559] [DI:complement] >gp:[GI:g2293260] [LN:AF008220] [AC:AF008220] [PN:DNA-polymerase III alpha-chain] [GN:dnaE] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis rrnB-dnaB genomic region.] [LE:184508] [RE:187855] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000993_7244012_c1_723	2336	6108	1287	428	1768	3.3e-182

Description

gp:[GI:e320380:g2168132] [LN:BIISOCIT] [AC:Y13358] [PN:isocitrate dehydrogenase] [OR:Bacillus israeli] [DB:genpept-bct1] [DE:Bacillus israeli isocitrate dehydrogenase gene.] [LE:242] [RE:1519] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000993_785952_c1_688	2337	6109	459	152	380	4.0e-35

Description

pir:[LN:A69999] [AC:A69999] [PN:phenylalanyl-tRNA synthetase (beta subunit) homolog ytpR] [GN:ytpR] [CL:Mycoplasma genitalium hypothetical protein MG449] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1185855:g2635466] [LN:BSUB0016] [AC:Z99119:AL009126] [GN:ytpR] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.] [NT:similar to phenylalanyl-tRNA synthetase (beta) [LE:54055] [RE:54660] [DI:complement] >gp:[GI:g2293213] [LN:AF008220] [AC:AF008220] [PN:YtpR] [GN:ytpR] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis rrnB-dnaB genomic region.] [NT:similarity to phenylalanine tRNA ligase of E. coli] [LE:125766] [RE:126371] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000993_803393_c3_947	2338	6110	732	243	536	1.2e-51
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Description

pir:[LN:H69407] [AC:H69407] [PN:conserved hypothetical protein AF1265] [CL:conserved hypothetical protein MJ1163] [OR:Archaeoglobus fulgidus] [DB:pir2] >gp:[GI:g2649315] [LN:AE001017] [AC:AE001017:AE000782] [PN:conserved hypothetical protein] [GN:AF1265] [OR:Archaeoglobus fulgidus] [DB:genpept-bct2] [DE:Archaeoglobus fulgidus section 90 of 172 of the complete genome.] [NT:similar to GB:L77117 PID:1591789 percent identity:] [LE:9248] [RE:9943] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000993_817555_f2_358	2339	6111	447	148		
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000993_824086_c3_952	2340	6112	882	293	859	7.0e-86
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Description

pir:[LN:G70001] [AC:G70001] [PN:acetyl-CoA carboxylase homolog yttI] [GN:yttI] [CL:acetyl-CoA carboxylase, carboxyltransferase beta chain] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1184170:g2635386] [LN:BSUB0015] [AC:Z99118:AL009126] [GN:yttI] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.] [NT:similar to acetyl-CoA carboxylase] [LE:192636] [RE:193424] [DI:complement] >gp:[GI:g2293262] [LN:AF008220] [AC:AF008220] [PN:acetyl-CoA carboxylase subunit] [GN:yttI] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis rrnB-dnaB genomic region.] [LE:189643] [RE:190431] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000993_82562_f3_523	2341	6113	1110	369	680	6.5e-67

Description

pir:[LN:H69758] [AC:H69758] [PN:proline oxidase homolog ycgM] [GN:ycgM] [CL:proline dehydrogenase homolog yusM] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1182272:g2632606] [LN:BSUB0002] [AC:Z99105:AL009126] [GN:ycgM] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 2 of 21): from 194651 to 415810.] [NT:similar to proline oxidase] [LE:149473] [RE:150384] [DI:direct] >gp:[GI:d1009589:g1805392] [LN:D50453] [AC:D50453] [GN:ycgM] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:168 trpC2) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis DNA for 25-36 degree region containing theamyE-srfA region, complete cds.] [LE:23774] [RE:24685] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000993_867187_c3_851	2342	6114	126	41		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000993_954768_c3_892	2343	6115	1053	350	611	1.3e-59

Description

sp:[LN:RIBG\_BACSU] [AC:P17618] [GN:RIBG] [OR:BACILLUS SUBTILIS] [EC:3.5.4.-] [DE:RIBOFLAVIN-SPECIFIC DEAMINASE,] [SP:P17618] [DB:swissprot] >pir:[LN:PN0100] [AC:S45543:PN0100:E69692] [PN:riboflavin-specific deaminase ribG] [GN:ribG] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:g410125] [LN:BACDIA] [AC:L09228] [GN:ribG] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain 168, sub\_species Marburg) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis spoVA to serA region.] [LE:8266] [RE:9351] [DI:direct] >gp:[GI:g40085] [LN:BSRIB] [AC:X51510] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B. subtilis riboflavin biosynthesis operon ribG, ribB, ribA, ribH, and ribT genes.] [NT:ribG protein product (AA 1-361)] [SP:P17618] [LE:1212] [RE:2297] [DI:direct] >gp:[GI:e1185597:g2634763] [LN:BSUB0013] [AC:Z99116:AL009126] [PN:riboflavin-specific deaminase] [GN:ribG] [FN:riboflavin biosynthesis] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 13 of 21): from 2395261 to 2613730.] [SP:P17618] [LE:34232] [RE:35317] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000993_960012_c1_663	2344	6116	450	149	123	6.9e-08

Description

gp:[GI:g3283053] [LN:AF054173] [AC:AF054173] [PN:staphylococcal accessory regulator A homolog] [GN:sarA] [OR:Staphylococcus epidermidis] [DB:genpept-bct2] [DE:Staphylococcus epidermidis staphylococcal accessory regulator Ahomolog (sarA) gene, complete cds.] [LE:887] [RE:1261] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000993_961562_f3_433	2345	6117	126	41		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000993_9785187_c3_867	2346	6118	171	56		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000993_9845327_c1_648	2347	6119	192	63		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000993_9884378_c3_916	2348	6120	156	51		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000994_10240925_c2_505	2349	6121	252	83	65	0.024

Description

gp:[GI:di037669:g4126667] [LN:AB016427] [AC:AB016427] [PN:transmembrane protein] [GN:bacM] [OR:Bacillus licheniformis] [SR:Bacillus licheniformis (strain:ATCC 10716) DNA] [DB:genpept-bct1] [DE:Bacillus licheniformis genes for transmembrane protein, thioesterase II-like protein and bacitracin synthetase 1 (BA1), complete and partial cds.] [NT:putative] [LE:694] [RE:>1956] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000994_10553827_c3_663	2350	6122	216	71	132	7.6e-09

Description

pir:[LN:F69808] [AC:F69808] [PN:hypothetical protein yfkK] [GN:yfkK] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1182777:g2633111] [LN:BSUB0005] [AC:Z99108:AL009126] [GN:yfkK] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 5 of 21): from 802821 to 1011250.] [LE:58273] [RE:58488] [DI:complement] >gp:[GI:di024280:g2626823] [LN:D83967] [AC:D83967] [PN:YfkK] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:AC327) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis genomic DNA, 74 degree region.] [LE:9433] [RE:9648] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000994_11125052_c1_439	2351	6123	1497	498	1715	1.4e-176

Description

pir:[LN:D70008] [AC:D70008] [PN:nicotinate phosphoribosyltransferase homolog yueK] [GN:yueK] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1184252:g2635670] [LN:BSUB0017] [AC:Z99120:AL009126] [GN:yueK] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 17 of 21): from 3197001 to 3414420.] [NT:similar to nicotinate phosphoribosyltransferase] [LE:61479] [RE:62951] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000994_11755317_c3_655	2352	6124	759	252	135	4.4e-07

Description

pir:[LN:G70045] [AC:G70045] [PN:hypothetical protein yvqF] [GN:yvqF] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1249815:g2832819] [LN:BS43KBDNA] [AC:AJ223978] [PN:YvqF protein] [GN:yvqF] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis 42.7kB DNA fragment from yvsA to yvqA.] [LE:31389] [RE:32114] [DI:direct] >gp:[GI:e1184389:g2635807] [LN:BSUB0017] [AC:Z99120:AL009126] [GN:yvqF] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 17 of 21): from 3197001 to 3414420.] [LE:198173] [RE:198898] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000994_117687_c1_441	2353	6125	1377	458	1704	2.0e-175

Description

sp: [LN:PUR8\_BACSU] [AC:P12047] [GN:PURB:PURE] [OR:BACILLUS SUBTILIS] [EC:4.3.2.2] [DE:ADENYLOSUCCINATE LYASE, (ADENYLOSUCCINASE) (ASL)] [SP:P12047] [DB:swissprot] >pir: [LN:WZBSDS] [AC:C29326:A69684] [PN:adenylosuccinate lyase,] [GN:purB] [CL:fumarate hydratase] [OR:Bacillus subtilis] [EC:4.3.2.2] [DB:pir1] [MP:18 min] >gp: [GI:g143366] [LN:BACPURF] [AC:J02732:K00047] [OR:Bacillus subtilis] [SR:B.subtilis (strain DE1 (prototroph DER. or W168)) DNA, clone pPZ] [DB:genpept-bct1] [DE:B.subtilis pur operon encoding purine biosynthesis enzymes, 12genes.] [NT:adenylosuccinate lyase (PUR-B)] [LE:2056] [RE:3351] [DI:direct] >gp: [GI:e1182624:g2632958] [LN:BSUB0004] [AC:Z99107:AL009126] [PN:adenylosuccinate lyase] [GN:purB] [FN:purine biosynthesis] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:4.3.2.2] [DE:Bacillus subtilis complete genome (section 4 of 21): from 600701 to 813890.] [SP:P12047] [LE:99038] [RE:100333] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000994_11959438_c2_534	2354	6126	135	44		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000994_1214075_f3_332	2355	6127	507	168	328	1.3e-29

Description

gp: [GI:g4981674] [LN:AE001770] [AC:AE001770:AE000512] [PN:ferritin] [GN:TM1128] [OR:Thermotoga maritima] [DB:genpept-bct2] [DE:Thermotoga maritima section 82 of 136 of the complete genome.] [NT:similar to GB:AE000782 percent identity: 71.95;] [LE:15936] [RE:16430] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000994_12142768_f1_9	2356	6128	300	99	110	4.2e-06

Description

pir: [LN:D71245] [AC:D71245] [PN:hypothetical protein PH0221] [GN:PH0221] [OR:Pyrococcus horikoshii] [DB:pir2] >gp: [GI:d1030234:g3256608] [LN:AP000001] [AC:AP000001:AB009465:AB009464:AB009466:AB009467:AB009468:AB009469] [PN:235aa long hypothetical protein] [GN:PH0221] [OR:Pyrococcus horikoshii] [SR:Pyrococcus horikoshii (strain:OT3) DNA] [DB:genpept-bct1] [DE:Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt. position (1/7).] [LE:194212] [RE:194919] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000994_12270011_f2_269	2357	6129	180	59	239	3.5e-20

Description

gp: [GI:e1311097:g3320009] [LN:SEHLDGN] [AC:Z49220] [GN:agrD] [OR:Staphylococcus epidermidis] [DB:genpept-bct1] [DE:Staphylococcus epidermidis hld and agr [A,B,C,D] genes.] [LE:1327] [RE:1467] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000994_12531558_f3_283	2358	6130	351	116		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000994_12603166_f3_301	2359	6131	303	100	100	1.9e-05

Description

pir: [LN:G71244] [AC:G71244] [PN:hypothetical protein PH0217] [GN:PH0217] [OR:Pyrococcus horikoshii] [DB:pir2] >gp: [GI:d1030229:g3256603] [LN:AP000001] [AC:AP000001:AB009465:AB009464:AB009466:AB009467:AB009468:AB009469] [PN:106aa long hypothetical protein] [GN:PH0217] [OR:Pyrococcus horikoshii] [SR:Pyrococcus horikoshii (strain:OT3) DNA] [DB:genpept-bct1] [DE:Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt. position (1/7).] [LE:191072] [RE:191392] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000994_1287557_f1_56	2360	6132	213	70		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000994_13678131_f3_393	2361	6133	840	279	299	1.5e-26

Description

pir: [LN:E69787] [AC:E69787] [PN:hypothetical protein ydiL] [GN:ydiL] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1182580:g2632914] [LN:BSUB0004] [AC:Z99107:AL009126] [GN:ydiL] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 4 of 21): from 600701 to 813890.] [LE:47946] [RE:48680] [DI:complement] >gp: [GI:d1020504:g1945117] [LN:D88802] [AC:D88802] [GN:ydiL] [OR:Bacillus subtilis] [SR:Bacillus subtilis (sub\_species:Marburg, strain:168, isolate:JH642) [DB:genpept-bct1] [DE:Bacillus subtilis DNA for phoB-rrnE-groESL region, complete cds.] [NT:transmembrane] [LE:34948] [RE:35682] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000994_1377337_c3_668	2362	6134	840	279	602	1.2e-58

Description

gp: [GI:g310603] [LN:STAORFPHI] [AC:L19300] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus (library: NCTC 8325) DNA] [DB:genpept-bct1] [DE:Staphylococcus aureus DNA sequence encoding three ORFs, completecds; prophage phi-11 sequence homology, 5' flank.] [LE:2651] [RE:3100] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000994_13837927_c2_518	2363	6135	1155	384	621	1.2e-60

Description

sp: [LN:TNPA\_STAAU] [AC:P06696] [GN:TNPA] [OR:STAPHYLOCOCCUS AUREUS] [DE:TRANSPOBASE A (TRANSPOSON TN554)] [SP:P06696] [DB:swissprot] >pir: [LN:A24584] [AC:A24584] [PN:transposition regulatory protein tnpA] [GN:tnpA] [OR:Staphylococcus aureus] [DB:pir2] >gp: [GI:g581277] [LN:ISTN554] [AC:X03216:K02987] [PN:tnpA protein] [GN:tnpA] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:Staphylococcus aureus transposon Tn554.] [NT:(aa 1-361)] [SP:P06696] [LE:134] [RE:1219] [DI:direct] >gp: [GI:d1046007:g5360831] [LN:D86934] [AC:D86934] [PN:transposaseA] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus (strain:N315) DNA, clone\_lib:library of N31] [DB:genpept] [DE:Staphylococcus aureus genes, mec region, partial and complete cds.] [NT:ORF N045; tnpA] [LE:29383] [RE:30468] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000994_13851088_c3_609	2364	6136	1089	362	185	6.2e-14

Description

gp: [GI:g1947171] [LN:CELE03H12] [AC:AF000299] [GN:E03H12.5] [OR:Caenorhabditis elegans] [SR:Caenorhabditis elegans strain=Bristol N2] [DB:genpept-inv2] [DE:Caenorhabditis elegans cosmid E03H12.] [NT:coded for by C. elegans cDNA yk170g3.5] [LE:1043:1176:1733] [RE:1131:1689:1762] [DI:directJoin]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000994_1385927_c1_442	2365	6137	711	236	851	4.9e-85

Description

sp: [LN:PCRB\_STAAU] [AC:Q53726] [OR:STAPHYLOCOCCUS AUREUS] [DE:PCRB PROTEIN] [SP:Q53726] [DB:swissprot] >pir: [LN:S39922] [AC:S39922:S27666] [PN:pcrB protein] [CL:pcrB protein] [OR:Staphylococcus aureus] [DB:pir2] >gp: [GI:g153061] [LN:STAPCRA] [AC:M63176] [GN:pcrA] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus (strain SA20) DNA] [DB:genpept-bct1] [DE:Staphylococcus aureus helicase required for T181 replication (pcrA) gene, complete cds.] [LE:256] [RE:939] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000994_1410277_f1_15	2366	6138	153	50		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000994_1414005_c1_477	2367	6139	579	192	324	3.4e-29

Description

pir: [LN:F69815] [AC:F69815] [PN:hypothetical protein ygaC] [GN:ygaC] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1182857:g2633191] [LN:BSUB0005] [AC:Z99108:AL009126] [GN:ygaC] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 5 of 21): from 802821 to 1011250.] [LE:135417] [RE:135734] [DI:direct] >gp: [GI:e281578:g1673391] [LN:BSZ82044] [AC:Z82044] [PN:hypothetical 12.2 kd protein] [GN:ygaC] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B. subtilis 25 kb genomic DNA segment (from sspE to katA).] [LE:2267] [RE:2584] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000994_14460882_c3_694	2368	6140	240	79	365	1.6e-33

Description

gp: [GI:g1022726] [LN:SHU35635] [AC:U35635] [PN:unknown] [OR:Staphylococcus haemolyticus] [SR:Staphylococcus haemolyticus strain=Y176] [DB:genpept-bct1] [DE:Staphylococcus haemolyticus IS1272 ORF1 and ORF2 genes, completecds.] [NT:ORF1] [LE:1101] [RE:1922] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000994_14460882_f2_232	2369	6141	126	41	99	9.9e-05

Description

gp: [GI:g1022726] [LN:SHU35635] [AC:U35635] [PN:unknown] [OR:Staphylococcus haemolyticus] [SR:Staphylococcus haemolyticus strain=Y176] [DB:genpept-bct1] [DE:Staphylococcus haemolyticus IS1272 ORF1 and ORF2 genes, completecds.] [NT:ORF1] [LE:1101] [RE:1922] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000994_14581306_f3_377	2370	6142	303	100	160	8.2e-12

Description

gp: [GI:g3676415] [LN:AF051917] [AC:AF051917:L19570] [PN:unknown] [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus plasmid pSK41, complete sequence.] [NT:Orf149] [LE:2068] [RE:2484] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000994_14642137_f3_381	2371	6143	168	55		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000994_14714077_c1_445	2372	6144	1209	402	715	1.3e-70

Description

pir: [LN:G69794] [AC:G69794] [PN:hypothetical protein yerH] [GN:yerH] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1182643:g2632977] [LN:BSUB0004] [AC:Z99107:AL009126] [GN:yerH] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 4 of 21): from 600701 to 813890.] [LE:122441] [RE:123631] [DI:direct] >gp: [GI:e1167977:g2577966] [LN:BSYERABCD] [AC:Y15254] [PN:YerH protein] [GN:yerH] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis 13kB DNA fragment, from yerA to sapB gene.] [LE:10086] [RE:11276] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000994_14845336_f1_44	2373	6145	147	48		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000994_14849093_c3_686	2374	6146	294	97	133	6.0e-09

Description

pir: [LN:F71245] [AC:F71245] [PN:hypothetical protein PHS004] [GN:PHS004] [OR:Pyrococcus horikoshii] [DB:pir2] >gp: [GI:d1030236:g3256610] [LN:AP000001] [AC:AP000001:AB009465:AB009464:AB009466:AB009467:AB009468:AB009469] [PN:58aa long hypothetical protein] [GN:PHS004] [OR:Pyrococcus horikoshii] [SR:Pyrococcus horikoshii (strain:OT3) DNA] [DB:genpept-bct1] [DE:Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt. position (1/7).] [NT:similar to GENPEPT:Z47547 percent identity:50.000] [LE:195255] [RE:195431] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000994_14883592_c1_429	2375	6147	2076	691	600	2.0e-58

Description

pir: [LN:S40098] [AC:S40098] [PN:hypothetical protein] [OR:Clostridium butyricum] [DB:pir2] >gp: [GI:g436133] [LN:CBPYFOLY] [AC:Z29084] [OR:Clostridium butyricum] [DB:genpept-bct1] [DE:C. butyricum transposon containing tbcC gene.] [NT:product is similar to TnpB of transposon Tn554 from] [LE:1088] [RE:3070] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000994_14900826_c2_587	2376	6148	351	116	188	8.9e-15

Description

gp: [GI:g208931] [LN:SYNORFLAC] [AC:M15619] [OR:synthetic construct] [SR:E.coli (strain SE5000) synthetic DNA, clone pKB1] [DB:genpept-syn] [DE:Synthetic E.coli ORF16/lacZ fusion protein, partial cds.] [NT:ORF16-lacZ fusion protein] [LE:29] [RE:>232] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000994_15033167_c3_671	2377	6149	126	41		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000994_15041430_c2_563	2378	6150	249	82		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000994_15121077_c1_448	2379	6151	1476	491	1626	3.7e-167

Description

pir: [LN:B69795] [AC:B69795] [PN:amidase homolog yerM] [GN:yerM] [CL:indoleacetamide hydrolase] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1182648:g2632982] [LN:BSUB0004] [AC:Z99107:AL009126] [GN:yerM] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 4 of 21): from 600701 to 813890.] [NT:alternate gene name: yedB; similar to amidase] [LE:127844] [RE:129301] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000994_16110257_f3_287	2380	6152	126	41		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000994_16209675_c3_674	2381	6153	159	52		

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	score	probability
AI7503000994_16219007_f3_366	2382	6154	921	306	1319	1.3e-134

#### Description

sp: [LN:BLAC\_STAAU] [AC:P00807] [GN:BLAZ] [OR:STAPHYLOCOCCUS AUREUS] [EC:3.5.2.6] [DE:BETA-LACTAMASE PRECURSOR, (PENICILLINASE)] [SP:P00807] [DB:swissprot] >pir: [LN:PNSAP] [AC:A01002:A23600:A90289:S06757:A45789:B45789:D45789::S11784:A60992] [PN:beta-lactamase, precursor:cephalosporinase:penicillinase] [GN:blaZ] [CL:beta-lactamase I] [OR:Staphylococcus aureus] [EC:3.5.2.6] [DB:pir1] >gp: [GI:g551850] [LN:ENEBELAA] [AC:M60253] [PN:beta-lactamase] [GN:blaZ] [OR:Enterococcus faecalis] [SR:Enterococcus faecalis (strain HH22) cDNA to mRNA] [DB:genpept-bct1] [EC:3.5.2.6] [DE:E.faecalis beta-lactamase mRNA, complete cds.] [LE:142] [RE:987] [DI:direct] >gp: [GI:g150717] [LN:PI25BLAZA] [AC:M15526] [PN:beta-lactamase] [GN:blaZ] [OR:Plasmid pI258] [SR:Plasmid pI258 (clone: pWN101) DNA] [DB:genpept-bct1] [EC:3.5.2.6] [DE:Plasmid pI258 (from S.aureus) beta-lactamase (blaZ), complete cds.] [LE:140] [RE:985] [DI:direct] >gp: [GI:g581568] [LN:SAPBLAZ] [AC:X04121] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:S. aureus PC1 beta-lactamase gene blaZ from plasmid pI258.] [NT:beta-lactamase (aa 1-281)] [SP:P00807] [LE:140] [RE:985] [DI:direct] >gp: [GI:g581590] [LN:SATN552] [AC:X52734] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:S.aureus Tn552 transposable element.] [NT:blaZ protein (AA 1-281)] [SP:P00807] [LE:5399] [RE:6244] [DI:direct] >gp: [GI:g581591] [LN:SATNBLAZ] [AC:X16471] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:Staphylococcus aureus transposon Tn4002 blaZ gene forbeta-lactamase.] [NT:beta-lactamase (AA 1-281)] [SP:P00807] [LE:142] [RE:987] [DI:direct] >gp: [GI:g1575125] [LN:SAU58139] [AC:U58139] [PN:beta-lactamase] [GN:blaZ] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus strain=a53] [DB:genpept-bct1] [DE:Staphylococcus aureus beta-lactamase (blaZ) gene, complete cds.] [LE:142] [RE:987] [DI:direct] >gp: [GI:g537336] [LN:STALACBAA] [AC:M25252] [PN:beta-lactamase] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus DNA] [DB:genpept-bct1] [DE:Staphylococcus aureus (clone pPC1) beta-lactamase gene, completecds.] [LE:123] [RE:968] [DI:direct] >gp: [GI:g537337] [LN:STALACBAB] [AC:M25253] [PN:beta-lactamase] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus DNA] [DB:genpept-bct1] [DE:Staphylococcus aureus (clone pS1) beta-lactamase gene, completecds.] [LE:29] [RE:874] [DI:direct]

ORF Name	NTID	AAID	NT Length	AA Length	score	probability
AI7503000994_16677343_c1_412	2383	6155	447	148	111	1.3e-06

#### Description

sp: [LN:Y357\_METJA] [AC:Q57803] [GN:MJ0357] [OR:METHANOCOCCUS JANNASCHII] [DE:HYPOTHETICAL PROTEIN MJ0357] [SP:Q57803] [DB:swissprot] >pir: [LN:E64344] [AC:E64344] [PN:hypothetical protein MJ0357] [OR:Methanococcus jannaschii] [DB:pir2] [MP:REV326407-325940] >gp: [GI:g1591066] [LN:U67489] [AC:U67489:L77117] [PN:M. jannaschii predicted coding region MJ0357] [GN:MJ0357] [OR:Methanococcus jannaschii] [DB:genpept-bct2] [DE:Methanococcus jannaschii section 31 of 150 of the complete genome.] [NT:hypothetical protein; identified by GeneMark;] [LE:1632] [RE:2099] [DI:complement]

ORF Name	NTID	AAID	NT Length	AA Length	score	probability
AI7503000994_16695300_f3_307	2384	6156	1113	370	586	5.9e-57

#### Description

pir: [LN:H69815] [AC:H69815] [PN:hypothetical protein ygaE] [GN:ygaE] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1182859:g2633193] [LN:BSUB0005] [AC:Z99108:AL009126] [GN:ygaE] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 5 of 21): from 802821 to 1011250.] [LE:137853] [RE:138914] [DI:complement] >gp: [GI:e281580:g1673393] [LN:BSZ82044] [AC:Z82044] [PN:hypothetical 40.7 kd protein] [GN:ygaE] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B. subtilis 25 kb genomic DNA segment (from sspE to katA).] [LE:4703] [RE:5764] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000994_19536693_c3_645	2385	6157	318	105	232	1.9e-19

Description

pir: [LN:A69795] [AC:A69795] [PN:conserved hypothetical protein yerL] [GN:yerL] [CL:probable glu-tRNA amidotransferase C chain] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:g2589194] [LN:AF008553] [AC:AF008553] [PN:Glu-tRNAGln amidotransferase subunit C] [GN:gatC] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis Glu-tRNAGln amidotransferase subunits C (gatC), A(gatA) and B (gatB) genes, complete cds.] [LE:412] [RE:702] [DI:direct] >gp: [GI:g2114425] [LN:BSU92466] [AC:U92466] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis strain JH642 amidase-like protein, partial cds, osmoregulated proline transporter (opuE) gene, complete cds and SapB (sapB) gene, partial cds.] [NT:similar to Synechocystis sp. hypothetical protein,] [LE:278] [RE:568] [DI:complement] >gp: [GI:e1182647:g2632981] [LN:BSUB0004] [AC:Z99107:AL009126] [GN:yerL] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 4 of 21): from 600701 to 813890.] [NT:alternate gene name: yedA; similar to hypothetical] [LE:127538] [RE:127828] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000994_19570253_f2_152	2386	6158	213	70		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000994_1958183_f1_121	2387	6159	648	215	976	2.8e-98

Description

gp: [GI:e1311096:g3320008] [LN:SEHLDGN] [AC:Z49220] [GN:agrB] [OR:Staphylococcus epidermidis] [DB:genpept-bct1] [DE:Staphylococcus epidermidis hld and agr[A,B,C,D] genes.] [LE:759] [RE:1343] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000994_1972278_f3_306	2388	6160	300	99	316	2.4e-28

Description

sp: [LN:GSAB\_BACSU] [AC:P71084] [GN:GSAB] [OR:BACILLUS SUBTILIS] [EC:5.4.3.8] [DE:(GLUTAMATE-1-SEMALDEHYDE AMINOTRANSFERASE) (GSA-AT)] [SP:P71084] [DB:swissprot] >gp: [GI:e281581:g1673394] [LN:BSZ82044] [AC:Z82044] [PN:glutamate-1-semialdehyde aminotransferase] [GN:gsaB] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B. subtilis 25 kb genomic DNA segment (from sspE to katA).] [SP:P71084] [LE:5984] [RE:7273] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000994_1988811_c3_672	2389	6161	1083	360	779	2.1e-77

Description

pir: [LN:A69802] [AC:A69802] [PN:A/G-specific adenine glycosylase homolog yfhQ] [GN:yfhQ] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1182852:g2633186] [LN:BSUB0005] [AC:Z99108:AL009126] [GN:yfhQ] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 5 of 21): from 802821 to 1011250.] [NT:similar to A/G-specific adenine glycosylase] [LE:132342] [RE:133451] [DI:direct] >gp: [GI:d1025399:g2804547] [LN:D85082] [AC:D85082] [PN:YfhQ] [OR:Bacillus subtilis] [SR:Bacillus subtilis DNA] [DB:genpept-bct1] [DE:Bacillus subtilis DNA, genome sequence, 79 to 81 degree region.] [LE:25233] [RE:26342] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000994_20100206_f2_137	2390	6162	165	54		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000994_20344411_c2_508	2391	6163	336	111	440	1.8e-41

Description

sp: [LN:CH10\_STAEP] [AC:P48227] [GN:GROES:HSP10] [OR:STAPHYLOCOCCUS EPIDERMIDIS] [DE:10] [SP:P48227] [DB:swissprot] >gp: [GI:g535341] [LN:SEU13618] [AC:U13618] [PN:heat shock protein 10] [GN:hsp10] [OR:Staphylococcus epidermidis] [DB:genpept-bct1] [DE:Staphylococcus epidermidis 9759 heat shock protein 10 (hsp10) and heat shock protein 60 (hsp60) genes, complete cds.] [LE:105] [RE:389] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000994_20348427_c2_578	2392	6164	126	41		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000994_2037838_f2_223	2393	6165	249	82	122	8.8e-08

Description

pir: [LN:A71136] [AC:A71136] [PN:hypothetical protein PH0853] [GN:PH0853] [CL:isoleucine--tRNA ligase] [OR:Pyrococcus horikoshii] [DB:pir2] >gp: [GI:d1030890:g3257264] [LN:AP000003] [AC:AP000003:AB009484:AB009485:AB009486:AB009487:AB009488:AB009489] [PN:134aa long hypothetical protein] [GN:PH0853] [OR:Pyrococcus horikoshii] [SR:Pyrococcus horikoshii (strain:OT3) DNA] [DB:genpept-bct1] [DE:Pyrococcus horikoshii OT3 genomic DNA, 544001-777000 nt. position(3/7).] [LE:216446] [RE:216850] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000994_20414052_f1_49	2394	6166	129	42		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000994_20735686_f1_87	2395	6167	957	318	853	3.0e-85

Description

sp: [LN:YYBQ\_BACSU] [AC:P37487] [GN:YYBQ] [OR:BACILLUS SUBTILIS] [DE:HYPOTHETICAL 34.0 KD PROTEIN IN COTF-TETB INTERGENIC REGION] [SP:P37487] [DB:swissprot] >pir: [LN:S65980] [AC:S65980:D70088] [PN:conserved hypothetical protein yybQ] [GN:yybQ] [CL:conserved hypothetical protein MJ0608] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:d1005728:g467340] [LN:BAC180K] [AC:D26185] [PN:unknown] [OR:Bacillus subtilis] [SR:Bacillus subtilis (sub\_species:Marburg, strain:168) DNA] [DB:genpept-bct1] [DE:B. subtilis DNA, 180 kilobase region of replication origin.] [LE:16200] [RE:17129] [DI:direct] >gp: [GI:e1184781:g2636602] [LN:BSUB0021] [AC:Z99124:AL009126] [GN:yybQ] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 21 of 21): from 3999281 to 4214814.] [NT:similar to hypothetical proteins] [SP:P37487] [LE:168132] [RE:169061] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000994_20881510_c2_510	2396	6168	492	163	216	9.6e-18

Description

gp: [GI:g3688823] [LN:AF084104] [AC:AF084104] [PN:hypothetical protein] [OR:Bacillus firmus] [DB:genpept-bct2] [DE:Bacillus firmus AcsA (acsA) gene, partial cds; SspA (sspA), hypothetical protein, maltose transportor ATP-binding protein(malK), leucine-rich protein transcriptional regulator (lrpR), hypothetical proteins, ABC transporter ATP-binding protein (natC), NatA (natA), NatB (natB), and hypothetical protein genes, completecds; and SpoIIJJ (spoIIJJ) gene, partial cds.] [NT:Orf15; similar to transcription regulator YtrA from] [LE:9870] [RE:10229] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000994_2125637_f3_294	2397	6169	150	49		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000994_21494536_c3_644	2398	6170	132	43		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000994_21516287_f1_17	2399	6171	135	44	100	1.9e-05

Description

pir: [LN:G64564] [AC:G64564] [PN:hypothetical protein HP0359] [OR:Helicobacter pylori] [DB:pir2] >gp: [GI:g2313473] [LN:AE000553] [AC:AE000553:AE000511] [PN:H. pylori predicted coding region HP0359] [GN:HP0359] [OR:Helicobacter pylori 26695] [DB:genpept-bct2] [DE:Helicobacter pylori 26695 section 31 of 134 of the complete genome.] [NT:hypothetical protein; identified by GeneMark;] [LE:250] [RE:315] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000994_21616078_c1_440	2400	6172	192	63	135	3.7e-09

Description

pir: [LN:C69792] [AC:C69792] [PN:hypothetical protein yebG] [GN:yebG] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:g2239294] [LN:BSU51115] [AC:U51115] [PN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis CotA (cotA), GabP (gabP), YeaB (yeaB), YeaC(yeaC), YebA (yebA), GMP synthetase (guA) genes, complete cds, andAIR carboxylase I (purE) gene, partial cds.] [NT:yebG] [LE:15312] [RE:15509] [DI:direct] >gp: [GI:e1182621:g2632955] [LN:BSUB0004] [AC:Z99107:AL009126] [GN:yebG] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 4 of 21): from 600701 to 813890.] [LE:96901] [RE:97098] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000994_21676433_c3_634	2401	6173	1137	378	192	3.3e-12

Description

gp: [GI:e1292355:g3127839] [LN:SC1A6] [AC:AL023496] [PN:hypothetical protein] [GN:SC1A6.07c] [OR:Streptomyces coelicolor] [DB:genpept-bct1] [DE:Streptomyces coelicolor cosmid 1A6.] [NT:SC1A6.07c, unknown, len: 813] [LE:7442] [RE:9070] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000994_22289077_c2_514	2402	6174	546	181		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000994_22688428_c2_584	2403	6175	144	47		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000994_23438461_c1_413	2404	6176	687	228	103	0.029

Description

gp: [GI:g5306158] [LN:AF160864] [AC:AF160864] [PN:orf1386] [GN:orf1386]  
 [OR:Mitochondrion Tetrahymena pyriformis] [SR:Tetrahymena pyriformis] [DB:genpept]  
 [DE:Tetrahymena pyriformis mitochondrial DNA, complete genome.] [NT:Open reading frame  
 ymf77 (CPGN); ATA initiation] [LE:22317] [RE:26477] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000994_23495437_f2_262	2405	6177	1305	434	1004	3.0e-101

Description

pir: [LN:JC4864] [AC:JC4864] [PN:aspartate transaminase,] [GN:aspAT] [OR:Bacillus circulans] [EC:2.6.1.1] [DB:pir2] >gp: [GI:e216734:g1147557] [LN:BCASPAMIN] [AC:X94433] [PN:Aspartate aminotransferase] [OR:Bacillus circulans subsp. alkalophilus] [DB:genpept-bct1] [EC:2.6.1.1] [DE:B.circulans aspartate aminotransferase gene.] [LE:367] [RE:1665] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000994_23572125_c2_571	2406	6178	534	177	393	1.7e-36

Description

sp: [LN:YKHA\_BACSU] [AC:P49851] [GN:YKHA] [OR:BACILLUS SUBTILIS] [DE:HYPOTHETICAL 20.1 KD PROTEIN IN HMP 5'REGION (ORF1)] [SP:P49851] [DB:swissprot]  
 >gp: [GI:d1011919:g1063246] [LN:BAC168TRP2] [AC:D78189] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:168trpC2) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis hmp DNA for 7 ORFs, complete cds.] [NT:low homology to P14 protein of Heamophilus] [LE:241] [RE:780] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000994_23595386_c1_484	2407	6179	627	208	271	1.4e-23

Description

pir: [LN:H70032] [AC:H70032] [PN:glycerate dehydrogenase homolog yvcT] [GN:yvcT] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1186156:g2635981] [LN:BSUB0018] [AC:Z99121:AL009126] [GN:yvcT] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.] [NT:similar to glycerate dehydrogenase] [LE:162076] [RE:163053] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000994_23600175_f2_274	2408	6180	123	40		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000994_23629202_c1_433	2409	6181	381	126	598	3.2e-58

Description

sp: [LN:BLAI\_STAAU] [AC:P18415] [GN:BLAI:PENI] [OR:STAPHYLOCOCCUS AUREUS] [DE:REPRESSOR PROTEIN] [SP:P18415] [DB:swissprot] >pir:[LN:S11782] [AC:S11782:S34446] [PN:regulatory protein blaI] [GN:blaI] [CL:regulatory protein blaI] [OR:Staphylococcus aureus] [DB:pir2] >gp:[GI:g46758] [LN:SATN552] [AC:X52734] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:S.aureus Tn552 transposable element.] [NT:blaI protein (AA 1-126)] [SP:P18415] [LE:3165] [RE:3545] [DI:complement] >gp:[GI:g152967] [LN:STABLA] [AC:M62650] [GN:blaI] [FN:putative blaZ repressor] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus DNA] [DB:genpept-bct1] [DE:Staphylococcus aureus blaZ gene, 5' end; blaR1 gene, complete cds; blaI gene, complete cds; and binR gene, 5' end.] [LE:1903] [RE:2283] [DI:direct] >gp:[GI:g152970] [LN:STABLAIA] [AC:M92376] [PN:beta-lactamase repressor] [GN:BlaI] [FN:represents the production of the blaZ product] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus (strain RN4) DNA] [DB:genpept-bct1] [DE:Staphylococcus aureus beta-lactamase repressor (BlaI) gene, complete cds.] [NT:no obvious promoters were found in the region] [LE:16] [RE:396] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000994_23672302_f3_302	2410	6182	156	51		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000994_23672562_c1_411	2411	6183	297	98	86	0.0034

Description

gp:[GI:e8900:g1335718] [LN:PFRESAR1] [AC:X05182] [PN:ring-infected erythrocyte surface antigen] [GN:RESA] [OR:Plasmodium falciparum] [SR:malaria parasite P. falciparum] [DB:genpept-inv1] [DE:P.falciparum FC27 Ag46 RESA mRNA for ring-infected erythrocytesurface antigen.] [SP:P13830] [LE:<1] [RE:>955] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000994_23727212_f2_175	2412	6184	303	100	87	0.00045

Description

pir:[LN:B69818] [AC:B69818] [PN:conserved hypothetical protein yhaH] [GN:yhaH] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1183002:g2633336] [LN:BSUB0006] [AC:Z99109:AL009126] [GN:yhaH] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 6 of 21): from 999501 to 1209940.] [NT:similar to hypothetical proteins from B. subtilis] [LE:73870] [RE:74226] [DI:complement] >gp:[GI:e325179:g2226119] [LN:BSY14077] [AC:Y14077] [PN:Hypothetical protein] [GN:yhaH] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis 10.6 Kb chromosomal DNA: glyB-prsA region.] [LE:6687] [RE:7043] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000994_23727250_f3_362	2413	6185	1395	464	1167	1.6e-118
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Description

sp: [LN:DHA2\_BACSU] [AC:P39616] [GN:YWDH:IPA-58R] [OR:BACILLUS SUBTILIS] [EC:1.2.1.3] [DE:PROBABLE ALDEHYDE DEHYDROGENASE YWDH,] [SP:P39616] [DB:swissprot] >pir:[LN:S39713] [AC:S39713:C70054] [PN:aldehyde dehydrogenase homolog ywdH:protein ipa-58r] [GN:ywdH] [CL:aldehyde dehydrogenase (NAD<sup>+</sup>):aldehyde dehydrogenase homology] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:g413982] [LN:BSGENR] [AC:X73124] [GN:ipa-58r] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B. subtilis genomic region (325 to 333).] [SP:P39616] [LE:59908] [RE:61281] [DI:complement] >gp:[GI:e1186295:g2636331] [LN:BSUB0020] [AC:Z99123:AL009126] [GN:ywdH] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 20 of 21): from 3798401 to 4010550.] [NT:alternate gene name: ipa-58r; similar to aldehyde] [SP:P39616] [LE:96681] [RE:98054] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000994_2379658_f2_144	2414	6186	225	74		
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000994_23850907_f1_109	2415	6187	201	66		
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000994_24017175_f2_202	2416	6188	150	49		
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000994_24218791_f1_86	2417	6189	588	195	525	1.7e-50
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Description

pir:[LN:C70008] [AC:C70008] [PN:pyrazinamidase/nicotinamidase homolog yueJ] [GN:yueJ] [CL:hypothetical protein b1011] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1184253:g2635671] [LN:BSUB0017] [AC:Z99120:AL009126] [GN:yueJ] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 17 of 21): from 3197001 to 3414420.] [NT:similar to pyrazinamidase/nicotinamidase] [LE:62967] [RE:63518] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000994_24225632_f2_253	2418	6190	171	56		
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000994_24257827_c2_511	2419	6191	387	128		
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000994_24265676_f1_120	2420	6192	144	47		

Description

NO-HIT

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000994_24350953_f2_151	2421	6193	132	43	72	0.017

Description

pir:[LN:G71244] [AC:G71244] [PN:hypothetical protein PH0217] [GN:PH0217]  
 [OR:Pyrococcus horikoshii] [DB:pir2] >gp:[GI:d1030229:g3256603] [LN:AP000001]  
 [AC:AP000001:AB009465:AB009464:AB009466:AB009467:AB009468:AB009469] [PN:106aa long  
 hypothetical protein] [GN:PH0217] [OR:Pyrococcus horikoshii] [SR:Pyrococcus horikoshii  
 (strain:OT3) DNA] [DB:genpept-bct1] [DE:Pyrococcus horikoshii OT3 genomic DNA, 1-287000  
 nt. position (1/7).] [LE:191072] [RE:191392] [DI:complement]

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000994_24353382_c3_608	2422	6194	1623	540	2592	1.6e-269

Description

gp:[GI:g535342] [LN:SEU13618] [AC:U13618] [PN:heat shock protein 60] [GN:hsp60]  
 [OR:Staphylococcus epidermidis] [DB:genpept-bct1] [DE:Staphylococcus epidermidis 9759  
 heat shock protein 10 (hsp10) and heat shock protein 60 (hsp60) genes, complete cds.]  
 [LE:445] [RE:2064] [DI:direct]

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000994_24407787_c1_483	2423	6195	354	117	84	0.029

Description

sp:[LN:SERX\_YEAST] [AC:P40054] [GN:YER081W] [OR:SACCHAROMYCES CEREVISIAE] [SR:, BAKER'S  
 YEAST] [EC:1.1.1.95] [DE:(PGDH)] [SP:P40054] [DB:swissprot] >pir:[LN:S50584] [AC:S50584  
 ] [PN:probable phosphoglycerate dehydrogenase, YER081w] [OR:Saccharomyces cerevisiae]  
 [EC:1.1.1.95] [DB:pir2] [MP:5R]

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000994_24415942_c2_516	2424	6196	840	279		

Description

NO-HIT

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000994_24475252_c2_533	2425	6197	162	53		

Description

NO-HIT

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000994_24475252_f1_2	2426	6198	159	52		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000994_24885938_c3_639	2427	6199	642	213	302	7.4e-27

Description

pir: [LN:B69792] [AC:B69792] [PN:hypothetical protein yebF] [GN:yebF] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:g2239293] [LN:BSU51115] [AC:U51115] [PN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis CotA (cotA), GabP (gabP), YeaB (yeaB), YeaC(yeaC), YebA (yebA), GMP synthetase (guaA) genes, complete cds, andAIR carboxylase I (purE) gene, partial cds.] [NT:yebF] [LE:15046] [RE:15312] [DI:direct] >gp: [GI:e1182620:g2632954] [LN:BSUB0004] [AC:Z99107:AL009126] [GN:yebF] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 4 of 21): from 600701 to 813890.] [LE:96635] [RE:96901] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000994_25428507_c1_457	2428	6200	576	191	109	0.0063
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Description

pir: [LN:G71609] [AC:G71609] [PN:hypothetical protein PFB0650w] [GN:PFB0650w] [OR:Plasmodium falciparum] [DB:pir2] >gp: [GI:g3845240] [LN:AE001408] [AC:AE001408:AE001362] [PN:hypothetical protein] [GN:PFB0650w] [OR:Plasmodium falciparum] [SR:malaria parasite P. falciparum] [DB:genpept-inv2] [DE:Plasmodium falciparum chromosome 2, section 45 of 73 of thecomplete sequence.] [NT:predicted by GlimmerM] [LE:4458] [RE:11960] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000994_25595387_f1_93	2429	6201	432	143	326	2.1e-29
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Description

gp: [GI:g3676415] [LN:AF051917] [AC:AF051917:L19570] [PN:unknown] [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus plasmid pSK41, complete sequence.] [NT:Orf149] [LE:2068] [RE:2484] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000994_25603388_f1_122	2430	6202	1293	430	2112	1.2e-218
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Description

gp: [GI:g2981295] [LN:AF012132] [AC:AF012132] [PN:histidine kinase] [GN:agrC] [OR:Staphylococcus epidermidis] [DB:genpept-bct2] [DE:Staphylococcus epidermidis agr system including response regulator(agrA), histidine kinase (agrC), AgrD (agrD), AgrB (agrB) and deltaxin (hld) genes, complete cds.] [NT:Agc; similar to S. aureus and S. lugdunensis AgrC] [LE:975] [RE:2264] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000994_256265_c2_564	2431	6203	1092	363	538	7.3e-52
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Description

pir: [LN:F70045] [AC:F70045] [PN:two-component sensor histidine kinase homolog yvqE] [GN:yvqE] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1249816:g2832820] [LN:BS43KBDNA] [AC:AJ223978] [PN:YvqE protein] [GN:yvqE] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis 42.7kB DNA fragment from yvsA to yvqA.] [LE:32111] [RE:33193] [DI:direct] >gp: [GI:e1184388:g2635806] [LN:BSUB0017] [AC:Z99120:AL009126] [GN:yvqE] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 17 of 21): from 3197001 to 3414420.] [NT:similar to two-component sensor histidine kinase] [LE:197094] [RE:198176] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000994_25678438_c2_583	2432	6204	474	157	334	3.0e-30

Description

pir:[LN:E70344] [AC:E70344] [PN:conserved hypothetical protein aq\_495] [GN:aq\_495] [CL:bacterioferritin comigratory protein:alkyl hydroperoxidase c22 protein homology] [OR:Aquifex aeolicus] [DB:pir2] >gp:[GI:g2983147] [LN:AE000692] [AC:AE000692:AE000657] [PN:hypothetical protein] [GN:aq\_495] [OR:Aquifex aeolicus] [DB:genpept-bct2] [DE:Aquifex aeolicus section 24 of 109 of the complete genome.] [LE:11182] [RE:11667] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000994_25781392_f1_54	2433	6205	1029	342	225	5.7e-17

Description

pir:[LN:H69815] [AC:H69815] [PN:hypothetical protein ygaE] [GN:ygaE] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1182859:g2633193] [LN:BSUB0005] [AC:Z99108:AL009126] [GN:ygaE] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 5 of 21): from 802821 to 1011250.] [LE:137853] [RE:138914] [DI:complement] >gp:[GI:e281580:g1673393] [LN:BSZ82044] [AC:Z82044] [PN:hypothetical 40.7 kd protein] [GN:ygaE] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B. subtilis 25 kb genomic DNA segment (from sspE to katA).] [LE:4703] [RE:5764] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000994_25790718_c2_541	2434	6206	315	104	349	7.7e-32

Description

pir:[LN:B69794] [AC:B69794] [PN:hypothetical protein yerC] [GN:yerC] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:g2465565] [LN:AF011544] [AC:AF011544] [PN:YecD] [GN:yecD] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis phosphoribosylaminoimidazole-carboxamideformyltransferase (purH-J) gene, partial cds, phosphoribosylglycinamide synthetase (purD), YecA (yecA), putativeadenine deaminase (yecB), YecC (yecC), and YecD (yecD) genes,complete cds, and putative glutamate synthase (yecE) gene, partialcds.] [NT:no apparent homology has been identified] [LE:6547] [RE:6861] [DI:direct] >gp:[GI:e1182638:g2632972] [LN:BSUB0004] [AC:Z99107:AL009126] [GN:yerC] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 4 of 21): from 600701 to 813890.] [LE:115237] [RE:115551] [DI:direct] >gp:[GI:e1167973:g2577962] [LN:BSYERABCD] [AC:Y15254] [PN:YerC protein] [GN:yerC] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis 13kB DNA fragment, from yerA to sapB gene.] [LE:2882] [RE:3196] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000994_26177163_c1_466	2435	6207	1272	423	971	9.5e-98

Description

sp:[LN:AMPS\_BACSU] [AC:P39762] [GN:AMPS] [OR:BACILLUS SUBTILIS] [EC:3.4.11.-] [DE:AMINOPEPTIDASE AMPS,] [SP:P39762] [DB:swissprot] >pir:[LN:C69585] [AC:C69585] [PN:aminopeptidase ampS] [GN:ampS] [CL:Bacillus aminopeptidase] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1185035:g2633816] [LN:BSUB0008] [AC:Z99111:AL009126] [PN:aminopeptidase] [GN:ampS] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:3.4.11.-] [DE:Bacillus subtilis complete genome (section 8 of 21): from 1394791 to 1603020.] [SP:P39762] [LE:119612] [RE:120844] [DI:complement] >gp:[GI:g3282130] [LN:AF012285] [AC:AF012285:AF012284:U51911] [PN:aminopeptidase] [GN:ampS] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis mobA-nprE gene region.] [NT:similar to ampS gene with GenBank Accession Number] [LE:20100] [RE:21332] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000994_26205151_f2_147	2436	6208	156	51	117	3.0e-07
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Description

pir:[LN:B71245] [AC:B71245] [PN:hypothetical protein PH0220] [GN:PH0220]  
 [OR:Pyrococcus horikoshii] [DB:pir2] >gp:[GI:d1030232:g3256606] [LN:AP000001]  
 [AC:AP000001:AB009465:AB009464:AB009466:AB009467:AB009468:AB009469] [PN:171aa long  
 hypothetical protein] [GN:PH0220] [OR:Pyrococcus horikoshii] [SR:Pyrococcus horikoshii  
 (strain:OT3) DNA] [DB:genpept-bct1] [DE:Pyrococcus horikoshii OT3 genomic DNA, 1-287000  
 nt. position (1/7).] [LE:192864] [RE:193379] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000994_26209510_c1_478	2437	6209	165	54		
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000994_26209577_f3_358	2438	6210	1068	355	892	2.2e-89
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Description

pir:[LN:C69811] [AC:C69811] [PN:nitric-oxide synthase homolog yf1M] [GN:yf1M]  
 [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1182753:g2633087] [LN:BSUB0005]  
 [AC:Z99108:AL009126] [GN:yf1M] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1]  
 [DE:Bacillus subtilis complete genome (section 5 of 21): from 802821 to 1011250.]  
 [NT:similar to nitric-oxide synthase] [LE:33422] [RE:34432] [DI:direct]  
 >gp:[GI:d1023169:g2443235] [LN:D86417] [AC:D86417] [PN:Yf1M] [OR:Bacillus subtilis]  
 [SR:Bacillus subtilis (strain:AC327) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis 35.7  
 kb genomic DNA, 70-73 degree region, complete cds.] [LE:14090] [RE:15100]  
 [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000994_26212875_c3_616	2439	6211	318	105		
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000994_26354787_c2_499	2440	6212	744	247	121	0.00043
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Description

gp:[GI:g3549261] [LN:AF057019] [AC:AF057019] [PN:interaptin] [GN:abpD]  
 [OR:Dictyostelium discoideum] [DB:genpept-inv2] [DE:Dictyostelium discoideum interaptin  
 (abpD) gene, complete cds.] [LE:1861:2796:7392] [RE:2378:7315:7570] [DI:directJoin]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000994_26369052_f1_91	2441	6213	141	46	101	1.5e-05
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Description

gp:[GI:g3676415] [LN:AF051917] [AC:AF051917:L19570] [PN:unknown] [OR:Staphylococcus  
 aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus plasmid pSK41, complete sequence.]  
 [NT:Orf149] [LE:2068] [RE:2484] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000994_26593808_f2_159	2442	6214	981	326	753	1.2e-74

Description

pir:[LN:H69801] [AC:H69801] [PN:hypothetical protein yfhP] [GN:yfhP] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1182851:g2633185] [LN:BSUB0005] [AC:Z99108:AL009126] [GN:yfhP] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 5 of 21): from 802821 to 1011250.] [LE:131143] [RE:132126] [DI:complement] >gp:[GI:d1025398:g2804546] [LN:D85082] [AC:D85082] [PN:YfhP] [OR:Bacillus subtilis] [SR:Bacillus subtilis DNA] [DB:genpept-bct1] [DE:Bacillus subtilis DNA, genome sequence, 79 to 81 degree region.] [LE:24034] [RE:25017] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503000994\_26689703\_c3\_679

2443 6215 453 150 562 2.1e-54

Description

sp:[LN:FUR3\_BACSU] [AC:P71086] [GN:YGAG] [OR:BACILLUS SUBTILIS] [DE:FERRIC UPTAKE REGULATION PROTEIN HOMOLOG 3] [SP:P71086] [DB:swissprot] >pir:[LN:B69816] [AC:B69816] [PN:transcription regulator Fur family homolog ygaG] [GN:ygaG] [CL:ferric uptake regulator] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1182862:g2633196] [LN:BSUB0005] [AC:Z99108:AL009126] [GN:ygaG] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 5 of 21): from 802821 to 1011250.] [NT:similar to transcriptional regulator (Fur family)] [SP:P71086] [LE:141173] [RE:141610] [DI:direct] >gp:[GI:e281583:g1673396] [LN:BSZ82044] [AC:Z82044] [PN:hypothetical 16.4 kd protein] [GN:ygaG] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B. subtilis 25 kb genomic DNA segment (from sspE to katA).] [NT:homology to ferric uptake regulation protein] [SP:P71086] [LE:8023] [RE:8460] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503000994\_26756500\_c3\_654

2444 6216 777 258 721 2.9e-71

Description

pir:[LN:E69810] [AC:E69810] [PN:methionine aminopeptidase homolog yflG] [GN:yflG] [CL:Escherichia coli methionyl aminopeptidase] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1182759:g2633093] [LN:BSUB0005] [AC:Z99108:AL009126] [GN:yflG] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 5 of 21): from 802821 to 1011250.] [NT:similar to methionine aminopeptidase] [LE:36423] [RE:37172] [DI:complement] >gp:[GI:d1023163:g2443229] [LN:D86417] [AC:D86417] [PN:YflG] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:AC327) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis 35.7 kb genomic DNA, 70-73 degree region, complete cds.] [LE:11350] [RE:12099] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503000994\_26757312\_f3\_321

2445 6217 1197 398 577 5.3e-56

Description

gp:[GI:e1423916:g4584097] [LN:BAJ10131] [AC:AJ010131] [GN:yfkH] [OR:Bacillus cereus] [DB:genpept-bct1] [DE:Bacillus cereus yfkH gene and partial ykvW, bc333c genes.] [LE:863] [RE:1732] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503000994\_285808\_f2\_146

2446 6218 225 74

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000994_29307187_c3_687	2447	6219	165	54		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000994_29500277_f3_392	2448	6220	171	56	169	9.2e-13

Description

gp: [GI:g1196510] [LN:MSGTCWPA] [AC:M15467] [PN:unknown protein] [OR:Mycobacterium tuberculosis] [SR:Mycobacterium tuberculosis (strain Erdman) DNA] [DB:genpept-bct1] [DE:M.tuberculosis 65 kDa antigen (cell wall protein a) gene.] [NT:ORF F175; putative] [LE:242] [RE:769] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000994_2992943_c1_425	2449	6221	624	207	382	2.5e-35

Description

gp: [GI:g4981569] [LN:AE001764] [AC:AE001764:AE000512] [PN:ABC transporter, ATP-binding protein] [GN:TM1028] [OR:Thermotoga maritima] [DB:genpept-bct2] [DE:Thermotoga maritima section 76 of 136 of the complete genome.] [NT:similar to GB:AE000782 percent identity: 60.48;] [LE:5922] [RE:6803] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000994_30265640_c3_693	2450	6222	1080	359	684	2.4e-67

Description

pir: [LN:E71373] [AC:E71373] [PN:probable regulatory protein (pfoS/R)] [GN:TP0038] [OR:Treponema pallidum subsp. pallidum] [SR:, syphilis spirochete] [DB:pir2] >gp: [GI:g3322295] [LN:AE001189] [AC:AE001189:AE000520] [PN:regulatory protein (pfoS/R)] [GN:TP0038] [OR:Treponema pallidum] [DB:genpept-bct2] [DE:Treponema pallidum section 5 of 87 of the complete genome.] [NT:similar to GP:1354775 percent identity: 100.00;] [LE:1177] [RE:2229] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000994_30506437_c2_517	2451	6223	177	58		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000994_30677268_c1_419	2452	6224	171	56		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000994_31273377_f1_113	2453	6225	171	56		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000994_3128452_c1_438	2454	6226	132	43		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000994_31289637_c2_545	2455	6227	123	40		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000994_31534456_c3_689	2456	6228	156	51		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000994_32037826_c1_451	2457	6229	1476	491	1119	2.0e-113

Description

pir: [LN:E69793] [AC:E69793] [PN:RNA methyltransferase homolog yefA] [GN:yefA] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1182653:g2632987] [LN:BSUB0004] [AC:Z99107:AL009126] [GN:yefA] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 4 of 21): from 600701 to 813890.] [NT:alternate gene name: yers; similar to RNA] [LE:136409] [RE:137788] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000994_3251577_c3_642	2458	6230	2190	729	3095	0.0

Description

sp: [LN:PCRA\_STAAU] [AC:Q53727] [GN:PCRA] [OR:STAPHYLOCOCCUS AUREUS] [EC:3.6.1.-] [DE:ATP-DEPENDENT HELICASE PCRA,] [SP:Q53727] [DB:swissprot] >pir: [LN:S39923] [AC:S39923:S27667] [PN:DNA helicase pcrA] [GN:pcrA] [CL:helicase II] [OR:Staphylococcus aureus] [DB:pir2] >gp: [GI:g153062] [LN:STAPCRA] [AC:M63176] [PN:helicase] [GN:pcrA] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus (strain SA20) DNA] [DB:genpept-bct1] [DE:Staphylococcus aureus helicase required for T181 replication (pcrA)gene, complete cds.] [LE:943] [RE:2970] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000994_32634387_f2_133	2459	6231	198	65		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000994_32680_c3_692	2460	6232	936	311	776	4.4e-77

Description

sp: [LN:STSP\_STAAU] [AC:P04188] [OR:STAPHYLOCOCCUS AUREUS] [EC:3.4.21.19] [DE:PROTEINASE] (V8 PROTEINASE) (ENDOPROTEINASE GLU-C) [SP:P04188] [DB:swissprot] >pir: [LN:PRSASK] [AC:A26812:A00966] [PN:glutamyl endopeptidase, precursor:staphylococcal serine proteinase] [CL:staphylococcal serine proteinase] [OR:Staphylococcus aureus] [EC:3.4.21.19] [DB:pir1] >gp: [GI:g46687] [LN:SASP] [AC:Y00356] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:Staphylococcus aureus V8 serine protease gene.] [NT:preproenzyme (AA -68 to 268)] [SP:P04188] [LE:354] [RE:1364] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000994_32689162_f3_397	2461	6233	807	268	1384	1.6e-141

Description

gp: [GI:g2981299] [LN:AF012132] [AC:AF012132] [PN:unknown] [GN:orf5] [OR:Staphylococcus epidermidis] [DB:genpept-bct2] [DE:Staphylococcus epidermidis agr system including response regulator(agrA), histidine kinase (agrC), AgrD (agrD), AgrB (agrB) and delta toxin (hld) genes, complete cds.] [NT:similar to S. aureus and S. lugdunensis orf5] [LE:3778] [RE:4572] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000994_32696088_c2_580	2462	6234	1749	582	1899	4.3e-196

Description

pir: [LN:G69815] [AC:G69815] [PN:ABC transporter (ATP-binding protein) homolog ygaD] [GN:ygaD] [CL:ATP-binding cassette homology] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1182858:g2633192] [LN:BSUB0005] [AC:Z99108:AL009126] [GN:ygaD] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 5 of 21): from 802821 to 1011250.] [NT:similar to ABC transporter (ATP-binding protein)] [LE:136007] [RE:137776] [DI:direct] >gp: [GI:e281579:g1673392] [LN:BSZ82044] [AC:Z82044] [PN:unidentified transporter-ATP binding] [GN:ygaD] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B. subtilis 25 kb genomic DNA segment (from sspE to katA).] [LE:2857] [RE:4626] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000994_33237786_f3_316	2463	6235	132	43		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000994_3330167_f3_398	2464	6236	132	43		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000994_33456965_c2_592	2465	6237	138	45		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000994_33463542_c1_487	2466	6238	180	59		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000994_3361326_c2_588	2467	6239	207	68		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000994_33631292_c1_461	2468	6240	414	137	84	0.048

Description

gp: [GI:g2182758] [LN:BBU42599] [AC:U42599] [OR: *Borrelia burgdorferi*] [SR: Lyme disease spirochete] [DB: genpept-bct1] [DE: *Borrelia burgdorferi* plasmid cp18, OspE (ospE) gene, partial cds.] [NT: OrfE] [LE: 1395] [RE: 1967] [DI: direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000994_33631626_c1_489	2469	6241	132	43		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000994_3392952_c1_410	2470	6242	591	196	195	1.6e-15

Description

gp: [GI:e247149:g1926347] [LN:LBPHIG1E] [AC:X98106] [GN: Rorf172] [OR: Bacteriophage phig1e] [DB: genpept-phg] [DE: *Lactobacillus* bacteriophage phig1e complete genomic DNA.] [LE: 29618] [RE: 30136] [DI: complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000994_34023427_c3_651	2471	6243	123	40		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000994_34164192_c3_640	2472	6244	138	45		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000994_34275325_c2_576	2473	6245	1521	506	238	5.0e-17

Description

sp: [LN:TAGH\_BACSU] [AC:P42954] [GN:TAGH] [OR:BACILLUS SUBTILIS] [DE:TEICHOIC ACID TRANSLOCATION ATP-BINDING PROTEIN TAGH] [SP:P42954] [DB:swissprot] >pir: [LN:S69203] [AC:S69203:A69721] [PN:teichoic acid translocation ATP-binding protein tagH] [GN:tagH] [CL:ATP-binding cassette homology] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:g755153] [LN:BSU13832] [AC:U13832] [PN:ATP-binding protein] [GN:tagH] [FN:teichoic acid translocation] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis 168 highly hydrophobic integral membrane protein(tagG) gene and ATP-binding protein (tagH) gene, complete cds.] [LE:1134] [RE:2717] [DI:direct] >gp: [GI:e1184476:g2636096] [LN:BSUB0019] [AC:Z99122:AL009126] [PN:ATP-binding protein] [GN:tagH] [FN:teichoic acid translocation] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.] [SP:P42954] [LE:75534] [RE:77117] [DI:complement] >gp: [GI:e1184476:g2636096] [LN:BSUB0019] [AC:Z99122:AL009126] [PN:ATP-binding protein] [GN:tagH] [FN:teichoic acid translocation] [OR:Bacillus subtilis] [DB:genpept] [DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.] [SP:P42954] [LE:75534] [RE:77117] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000994_34383400_c3_618	2474	6246	582	193	78	0.010

Description

gp: [GI:g4726117] [LN:ATAC006436] [AC:AC006436] [GN:F13J11.13] [OR:Arabidopsis thaliana] [SR:thale cress] [DB:genpept-pln2] [DE:Arabidopsis thaliana chromosome II BAC F13J11 genomic sequence,complete sequence.] [NT:unknown protein] [LE:50474] [RE:50725] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000994_34557262_c2_585	2475	6247	135	44		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000994_34572177_c2_513	2476	6248	735	244	147	1.5e-08

Description

pir: [LN:S42928] [AC:S42928] [PN:probable membrane-spanning protein] [OR:Staphylococcus epidermidis] [DB:pir2] >gp: [GI:g459263] [LN:SESTPSMP] [AC:Z30586] [PN:membrane spanning protein (putative)] [OR:Staphylococcus epidermidis] [DB:genpept-bct1] [DE:S.epidermidis (968) genes for potential ABC transporter and potential membrane spanning protein.] [LE:896] [RE:1666] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000994_34652177_c3_656	2477	6249	648	215	546	1.0e-52

Description

pir: [LN:E70045] [AC:E70045] [PN:two-component response regulator [YvqE] homolog yvqC] [GN:yvqC] [CL:regulatory protein comA:response regulator homology] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1249817:g2832821] [LN:BS43KBDNA] [AC:AJ223978] [PN:YvqC protein] [GN:yvqC] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis 42.7kB DNA fragment from yvsA to yvqA.] [LE:33171] [RE:33806] [DI:direct] >gp: [GI:e1184387:g2635805] [LN:BSUB0017] [AC:Z99120:AL009126] [GN:yvqC] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.] [NT:similar to two-component response regulator [YvqE]] [LE:196481] [RE:197116] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000994_35428128_c3_635	2478	6250	141	46		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000994_35443785_c2_562	2479	6251	207	68		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000994_35885_f3_383	2480	6252	504	167		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000994_36119093_c3_643	2481	6253	2001	666	2102	1.3e-217

Description

pir: [LN:F69794] [AC:F69794] [PN:DNA ligase (NAD+),] [GN:yerG]  
 [CL:polydeoxyribonucleotide synthase (NAD+)] [OR:Bacillus subtilis] [EC:6.5.1.2]  
 [DB:pir1] >gp: [GI:e1182642:g2632976] [LN:BSUB0004] [AC:Z99107:AL009126] [GN:yerG]  
 [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete  
 genome (section 4 of 21): from 600701 to 813890.] [NT:similar to DNA ligase] [LE:120419]  
 [RE:122425] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000994_36195250_f3_359	2482	6254	822	273	375	1.4e-34

Description

sp: [LN:PHEA\_METJA] [AC:Q58054] [GN:PHEA:MJ0637] [OR:METHANOCOCCUS JANNASCHII]  
 [EC:4.2.1.51] [DE:PROBABLE PREPHENATE DEHYDRATASE, (PDT)] [SP:Q58054] [DB:swissprot]  
 >pir: [LN:E64379] [AC:E64379] [PN:prephenate dehydratase,] [CL:prephenate  
 dehydratase:prephenate dehydratase homology] [OR:Methanococcus jannaschii]  
 [EC:4.2.1.51] [DB:pir2] [MP:REV567914-567096] >gp: [GI:g1591349] [LN:U67511]  
 [AC:U67511:L77117] [PN:chorismate mutase/prephenate dehydratase (pheA)] [GN:MJ0637]  
 [OR:Methanococcus jannaschii] [DB:genpept-bct2] [DE:Methanococcus jannaschii section 53  
 of 150 of the complete genome.] [NT:similar to SP:P43909 PID:683585 percent identity:]  
 [LE:7667] [RE:8485] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000994_36219692_c3_648	2483	6255	561	186	133	2.0e-08

Description

pir: [LN:A36886] [AC:A36886] [PN:surface protein PAg negative regulator par] [GN:par]  
 [OR:Streptococcus sobrinus] [DB:pir2] >gp: [GI:d1003084:g425488] [LN:STRREPRESP]  
 [AC:D13323] [PN:repressor protein] [GN:par] [OR:Streptococcus sobrinus]  
 [SR:Streptococcus sobrinus (strain MT3791) DNA, clone pPG11] [DB:genpept-bct1]  
 [DE:Streptococcus sobrinus gene for repressor protein of surfaceprotein antigen gene  
 (pag), complete cds.] [NT:This ORF2 starts at the GTG codon (position 1162)] [LE:1162]  
 [RE:1773] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000994_36220000_c2_525	2484	6256	1047	348	557	7.0e-54
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Description

pir: [LN:D69856] [AC:D69856] [PN:conserved hypothetical protein ykgB] [GN:ykgB] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1181502:g2632022] [LN:BSAJ2571] [AC:AJ002571] [PN:YkgB] [GN:ykgB] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis 168 56 kb DNA fragment between xlyA and ykoR.] [LE:22000] [RE:23049] [DI:complement] >gp: [GI:e1183321:g2633655] [LN:BSUB0007] [AC:Z99110:AL009126] [GN:ykgB] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 7 of 21): from 1194391 to 1411140.] [NT:similar to hypothetical proteins] [LE:174949] [RE:175998] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000994_36221013_f2_135	2485	6257	171	56		
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000994_36336012_c3_664	2486	6258	165	54		
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000994_36367302_c3_600	2487	6259	1564	187	122	2.7e-06
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Description

sp: [LN:Y359\_METJA] [AC:Q57805] [GN:MJ0359] [OR:METHANOCOCCUS JANNASCHII] [DE:HYPOTHETICAL PROTEIN MJ0359] [SP:Q57805] [DB:swissprot] >pir: [LN:G64344] [AC:G64344] [PN:hypothetical protein MJ0359] [OR:Methanococcus jannaschii] [DB:pir2] [MP:REV327449-326805] >gp: [GI:g1591068] [LN:U67489] [AC:U67489:L77117] [PN:M. jannaschii predicted coding region MJ0359] [GN:MJ0359] [OR:Methanococcus jannaschii] [DB:genpept-bct2] [DE:Methanococcus jannaschii section 31 of 150 of the complete genome.] [NT:hypothetical protein; identified by GeneMark;] [LE:2497] [RE:3141] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000994_36457341_c2_593	2488	6260	135	44	81	0.019
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Description

pir: [LN:S75730] [AC:S75730:S50064] [PN:8-amino-7-oxononanoate synthase, :7-keto-8-aminopelargonic acid synthetase:protein slr0917:7-keto-8-aminopelargonic acid synthetase:protein slr0917] [GN:bioF] [CL:5-aminolevulinate synthase] [OR:Synechocystis sp.] [SR:PCC 6803, , PCC 6803] [SR:PCC 6803, ] [EC:2.3.1.47] [DB:pir2] >gp: [GI:d1011116:g1673311] [LN:SYCSLLE] [AC:D64003:AB001339] [PN:7-keto-8-aminopelargonic acid synthetase] [GN:bioF] [OR:Synechocystis sp.] [SR:Synechocystis sp. (strain:PCC6803) DNA] [DB:genpept-bct1] [DE:Synechocystis sp. PCC6803 complete genome, 22/27, 2755703-2868766.] [NT:ORF\_ID:slr0917] [LE:35986] [RE:37299] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000994_36522175_f1_69	2489	6261	1557	518	2240	3.2e-232
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Description

gp: [GI:g2565311] [LN:AF024571] [AC:AF024571] [PN:high affinity proline permease] [GN:putP] [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus high affinity proline permease (putP) gene, complete cds.] [LE:339] [RE:1832] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000994_39077_f2_270	2490	6262	717	238	1223	1.9e-124
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Description

gp: [GI:g2981294] [LN:AF012132] [AC:AF012132] [PN:response regulator] [GN:agrA] [OR:Staphylococcus epidermidis] [DB:genpept-bct2] [DE:Staphylococcus epidermidis agr system including response regulator(agrA), histidine kinase (agrC), AgrD (agrD), AgrB (agrB) and delta toxin (hld) genes, complete cds.] [NT:AgrA; similar to S. aureus and S. lugdunensis AgrA] [LE:242] [RE:958] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000994_3939013_c2_573	2491	6263	210	69	109	2.1e-06
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Description

pir: [LN:C69807] [AC:C69807] [PN:hypothetical protein yfjT] [GN:yfjT] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1182787:g2633121] [LN:BSUB0005] [AC:Z99108:AL009126] [GN:yfjT] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 5 of 21): from 802821 to 1011250.] [LE:65959] [RE:66144] [DI:direct] >gp: [GI:d1024269:g2626812] [LN:D83967] [AC:D83967] [PN:YfjT] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:AC327) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis genomic DNA, 74 degree region.] [LE:1777] [RE:1962] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000994_3942015_c1_471	2492	6264	528	175	790	1.4e-78
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Description

sp: [LN:YLY1\_STAAU] [AC:Q53719] [OR:STAPHYLOCOCCUS AUREUS] [DE:HYPOTHETICAL 18.6 KD PROTEIN IN LYTA 3'REGION (ORF1)] [SP:Q53719] [DB:swissprot] >gp: [GI:g310602] [LN:STAORFPHI] [AC:L19300] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus (library: NCTC 8325) DNA] [DB:genpept-bct1] [DE:Staphylococcus aureus DNA sequence encoding three ORFs, completecds; prophage phi-11 sequence homology, 5' flank.] [LE:1798] [RE:2313] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000994_4021888_c3_615	2493	6265	669	222	83	0.0039
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Description

pir: [LN:D71114] [AC:D71114] [PN:hypothetical protein PH0683] [GN:PH0683] [OR:Pyrococcus horikoshii] [DB:pir2] >gp: [GI:d1030717:g3257091] [LN:AP000003] [AC:AP000003:AB009484:AB009485:AB009486:AB009487:AB009488:AB009489] [PN:107aa long hypothetical protein] [GN:PH0683] [OR:Pyrococcus horikoshii] [SR:Pyrococcus horikoshii (strain:OT3) DNA] [DB:genpept-bct1] [DE:Pyrococcus horikoshii OT3 genomic DNA, 544001-777000 nt. position(3/7).] [LE:63024] [RE:63347] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503000994_4062500_c2_507	2494	6266	1401	466	502	3.3e-47
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Description

gp: [GI:e1314011:g3393011] [LN:SAA224764] [AC:AJ224764] [PN:Clumping factor B] [GN:clfB] [FN:binds fibrinogen] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:Staphylococcus aureus strain Newman clumping factor B (clfB) gene.] [LE:28] [RE:2769] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503000994_4072936_c1_453	2495	6267	153	50		
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503000994_4093753_f3_387	2496	6268	126	41		
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503000994_4095277_c3_627	2497	6269	1827	608	2760	2.5e-287
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Description

pir: [LN:S11783] [AC:S11783:S27371:S34445] [PN:bla regulator protein blaR1:probable beta-lactam receptor signal transducer protein] [GN:blaR1] [CL:mecR1 protein:beta-lactamase OXA2 homology] [OR:Staphylococcus aureus] [DB:pir2] >gp: [GI:g152966] [LN:STABLA] [AC:M62650] [GN:blaR1] [FN:putative beta-lactam receptor-signal] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus DNA] [DB:genpept-bct1] [DE:Staphylococcus aureus blaZ gene, 5' end; blaR1 gene, complete cds; blaI gene, complete cds; and binR gene, 5' end.] [LE:156] [RE:1913] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503000994_409556_f1_10	2498	6270	135	44	112	2.5e-06
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Description

pir: [LN:D71245] [AC:D71245] [PN:hypothetical protein PH0221] [GN:PH0221] [OR:Pyrococcus horikoshii] [DB:pir2] >gp: [GI:d1030234:g3256608] [LN:AP000001] [AC:AP000001:AB009465:AB009464:AB009466:AB009467:AB009468:AB009469] [PN:235aa long hypothetical protein] [GN:PH0221] [OR:Pyrococcus horikoshii] [SR:Pyrococcus horikoshii (strain:OT3) DNA] [DB:genpept-bct1] [DE:Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt. position (1/7).] [LE:194212] [RE:194919] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503000994_4101517_f1_100	2499	6271	1068	355		
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000994_4179637_c3_622	2500	6272	387	128	207	8.6e-17

Description

sp: [LN:TRAC\_STAAU] [AC:P06698] [GN:TNPC] [OR:STAPHYLOCOCCUS AUREUS] [DE:TRANSPOSE FOR TRANSPOSON TN554] [SP:P06698] [DB:swissprot] >pir: [LN:C24584] [AC:C24584] [PN:transposition regulatory protein tnpC] [GN:tnpC] [CL:transposition regulatory protein tnpC] [OR:Staphylococcus aureus] [DB:pir2] >gp: [GI:g43729] [LN:ISTN554] [AC:X03216:K02987] [PN:pot. tnpC protein] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:Staphylococcus aureus transposon Tn554.] [NT:(aa 1-125)] [SP:P06698] [LE:3115] [RE:3492] [DI:direct] >gp: [GI:d1046009:g5360833] [LN:D86934] [AC:D86934] [PN:transposaseC] [GN:tnpC] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus (strain:N315) DNA, clone\_lib:library of N31] [DB:genpept] [DE:Staphylococcus aureus genes, mec region, partial and complete cds.] [NT:ORF N047] [LE:32364] [RE:32741] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000994_430325_c1_456	2501	6273	1383	460	649	1.3e-63

Description

gp: [GI:g3820539] [LN:AF080002] [AC:AF080002] [PN:UDP-N-acetylmuramyl tripeptide synthetase MurC] [GN:murC] [OR:Heliobacillus mobilis] [DB:genpept-bct2] [DE:Heliobacillus mobilis exopolyphosphatase Ppx (ppx) gene, partialcds; cobyric acid synthase CobQ (cobQ), UDP-N-acetylmuramyltripeptide synthetase MurC (murC), glutamyl tRNA reductase HemA(hemA), photosynthesis gene cluster, complete sequence, stage II sporulation protein E Sp2E (sp2E), cell cycle protein MesJ (mesJ), and ATP-dependent zinc metallopeptidase FtsH (ftsH) genes, completecds; and nucleoside diphosphate kinase B NdkB (ndkB) gene, partialcds.] [LE:2000] [RE:3367] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000994_4329635_f2_164	2502	6274	126	41		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000994_4689130_f2_272	2503	6275	306	101	81	0.029

Description

pir: [LN:A58932] [AC:A58932] [PN:cytochrome C-type biogenesis protein CCMF] [GN:yejR:ccmF] [OR:mitochondrion Cyanidioschyzon merolae] [DB:pir2] >gp: [GI:d1037513:g4115789] [LN:D89861] [AC:D89861] [PN:cytochrome C-type biogenesis protein CCMF] [GN:yejR or ccmF] [OR:Mitochondrion Cyanidioschyzon merolae] [SR:Cyanidioschyzon merolae (strain:10D) mitochondrial DNA] [DB:genpept-pln1] [DE:Cyanidioschyzon merolae mitochondrial DNA, complete sequence.] [LE:16296] [RE:18158] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000994_4722265_c1_472	2504	6276	858	285	416	6.1e-39

Description

pir: [LN:H69800] [AC:H69800] [PN:hypothetical protein yfhG] [GN:yfhG] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1182842:g2633176] [LN:BSUB0005] [AC:Z99108:AL009126] [GN:yfhG] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 5 of 21): from 802821 to 1011250.] [LE:122320] [RE:123114] [DI:direct] >gp: [GI:d1025389:g2804537] [LN:D85082] [AC:D85082] [PN:YfhG] [OR:Bacillus subtilis] [SR:Bacillus subtilis DNA] [DB:genpept-bct1] [DE:Bacillus subtilis DNA, genome sequence, 79 to 81 degree region.] [LE:15211] [RE:16005] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000994_4726566_f2_189	2505	6277	582	193	187	3.8e-13

Description

gp: [GI:g4981093] [LN:AE001732] [AC:AE001732:AE000512] [PN:DNA polymerase III, alpha subunit] [GN:TM0576] [OR:Thermotoga maritima] [DB:genpept-bct2] [DE:Thermotoga maritima section 44 of 136 of the complete genome.] [NT:similar to GB:M22996 SP:P13267 GB:M33543 GB:S55653] [LE:5720] [RE:9823] [DI:direct] >gp: [GI:g3930535] [LN:AF065313] [AC:AF065313] [PN:DNA polymerase III] [GN:polC] [OR:Thermotoga maritima] [DB:genpept-bct2] [DE:Thermotoga maritima DNA polymerase III (polC) gene, complete cds.] [NT:family C DNA polymerase] [LE:235] [RE:4338] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000994_4728377_f2_171	2506	6278	1146	381	544	1.7e-52

Description

pir: [LN:F69807] [AC:F69807] [PN:hypothetical protein yfkB] [GN:yfkB] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1182785:g2633119] [LN:BSUB0005] [AC:Z99108:AL009126] [GN:yfkB] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 5 of 21): from 802821 to 1011250.] [LE:64694] [RE:65155] [DI:complement] >gp: [GI:d1024271:g2626814] [LN:D83967] [AC:D83967] [PN:YfkB] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:AC327) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis genomic DNA, 74 degree region.] [LE:2766] [RE:3227] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000994_4876387_f3_376	2507	6279	180	59		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000994_4881313_c1_475	2508	6280	159	52		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000994_4900443_c1_449	2509	6281	1440	479	2460	1.5e-255

Description

sp: [LN:YZDD\_BACSU] [AC:Q45486] [GN:YZDD] [OR:BACILLUS SUBTILIS] [DE:PET112-LIKE PROTEIN] [SP:Q45486] [DB:swissprot] >gp: [GI:g1354211] [LN:BSU49790] [AC:U49790] [PN:PET112-like protein] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis PET112-like protein gene, complete cds.] [LE:433] [RE:1860] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000994_5133500_f1_48	2510	6282	480	159	358	8.6e-33

Description

pir: [LN:E69808] [AC:E69808] [PN:protein-tyrosine phosphatase homolog yfkJ] [GN:yfkJ] [CL:protein-tyrosine-phosphatase, low molecular weight] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1182778:g2633112] [LN:BSUB0005] [AC:Z99108:AL009126] [GN:yfkJ] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 5 of 21): from 802821 to 1011250.] [NT:similar to protein-tyrosine phosphatase] [LE:58691] [RE:59161] [DI:direct] >gp: [GI:d1024279:g2626822] [LN:D83967] [AC:D83967] [PN:YfkJ] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:AC327) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis genomic DNA, 74 degree region.] [LE:8760] [RE:9230] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000994_5167268_c3_649	2511	6283	1080	359	613	8.2e-60

Description

sp: [LN:DINP\_ECOLI] [AC:Q47155:Q47683] [GN:DINP] [OR:ESCHERICHIA COLI]  
 [DE:DNA-DAMAGE-INDUCIBLE PROTEIN P] [SP:Q47155:Q47683] [DB:swissprot] >pir: [LN:H64747]  
 [AC:H64747] [PN:DNA-damage-inducibile protein dinP] [GN:dinP] [CL:umuC protein]  
 [OR:Escherichia coli] [DB:pir2] >gp: [GI:d1008174:g984587] [LN:ECODINJ] [AC:D38582]  
 [PN:DinP] [OR:Escherichia coli] [SR:Escherichia coli (sub\_strain W3110, strain K-12)  
 (library: Kohara')] [DB:genpept-bct1] [DE:Escherichia coli genes for 'YafH, YafI, YafJ,  
 YafK, YafQ, DinJ, YafL, YafM, FhiA, MbhA, DinP, YafN, YafO and YafP.] [NT:hypothetical;  
 similarity to YLW6\_CAEEL (P34409),] [LE:8540] [RE:9595] [DI:direct]  
 >gp: [GI:d1041669:g4902967] [LN:ECOTSF] [AC:D83536] [PN:DNA-damage-inducible protein p.]  
 [GN:dinP] [OR:Escherichia coli] [SR:Escherichia coli (strain:K12) DNA]  
 [DB:genpept-bct1] [DE:Escherichia coli genomic DNA. (4.1 - 6.1 min).]  
 [INT:ORF\_ID:o127#9; similar to PIR Accession Number] [LE:60446] [RE:61501] [DI:direct]  
 >gp: [GI:g1552799] [LN:ECU70214] [AC:U70214] [PN:DinP] [GN:dinP] [OR:Escherichia coli]  
 [DB:genpept-bct1] [DE:Escherichia coli chromosome minutes 4-6.] [LE:81973] [RE:83028]  
 [DI:direct] >gp: [GI:g1786425] [LN:AE000131] [AC:AE000131:U00096] [PN:damage-inducible  
 protein P; putative tRNA] [GN:dinP] [FN:putative enzyme; Not classified]  
 [OR:Escherichia coli] [DB:genpept-bct2] [DE:Escherichia coli K-12 MG1655 section 21 of  
 400 of the complete genome.] [NT:o351; 100 pct identical to GB: ECODINJ\_11] [LE:7487]  
 [RE:8542] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000994_5269400_f3_291	2512	6284	138	45		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000994_570327_c1_424	2513	6285	171	56	52	0.026

Description

pir: [LN:S68156] [AC:S68156] [PN:NADH dehydrogenase (ubiquinone), chain 3] [GN:ND3]  
 [CL:NADH dehydrogenase (ubiquinone) chain 3] [OR:mitochondrion Dictyostelium  
 discoideum] [EC:1.6.5.3] [DB:pir2] >gp: [GI:d1041830:g4958885] [LN:AB000109]  
 [AC:AB000109] [PN:NADH dehydrogenase subunit 3] [GN:nad3] [OR:Mitochondrion  
 Dictyostelium discoideum] [SR:Dictyostelium discoideum (strain:AX3, partially X22  
 (48172-5151)] [DB:genpept-inv1] [EC:1.6.5.3] [DE:Dictyostelium discoideum mitochondrial  
 DNA, complete sequence.] [LE:24783] [RE:25145] [DI:direct] >gp: [GI:d1004450:g699592]  
 [LN:DDID16466] [AC:D16466] [PN:NADH dehydrogenase subunit 3] [GN:nad3]  
 [OR:Mitochondrion Dictyostelium discoideum] [SR:Dictyostelium discoideum (strain:AX3)  
 mitochondrial DNA] [DB:genpept-inv1] [EC:1.6.5.3] [DE:Dictyostelium discoideum  
 mitochondrial DNA.] [LE:7866] [RE:8228] [DI:direct] >gp: [GI:d1004450:g699592]  
 [LN:DDID16466] [AC:D16466] [PN:NADH dehydrogenase subunit 3] [GN:nad3]  
 [OR:Mitochondrion Dictyostelium discoideum] [SR:Dictyostelium discoideum (strain:AX3)  
 mitochondrial DNA] [DB:genpept] [EC:1.6.5.3] [DE:Dictyostelium discoideum mitochondrial  
 DNA.] [LE:7866] [RE:8228] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000994_5860052_f3_388	2514	6286	435	144	107	3.4e-06

Description

pir: [LN:H71190] [AC:H71190] [PN:hypothetical protein PH1800] [GN:PH1800] [OR:Pyrococcus horikoshii] [DB:pir2] >gp: [GI:d1031862:g3258236] [LN:AP000007] [AC:AP000007:AB009464:AB009465:AB009521:AB009522:AB009523:AB009524] [PN:133aa long hypothetical protein] [GN:PH1800] [OR:Pyrococcus horikoshii] [SR:Pyrococcus horikoshii (strain:OT3) DNA] [DB:genpept-bct1] [DE:Pyrococcus horikoshii OT3 genomic DNA, 1485001-1738505 nt. position(7/7).] [LE:80658] [RE:81059] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000994_5913882_f2_167	2515	6287	123	40		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000994_6053308_c2_538	2516	6288	903	300	815	3.2e-81

Description

sp: [LN:NADE\_ECOLI] [AC:P18843:P78235] [GN:NADE:EFG:NTRL] [OR:ESCHERICHIA COLI] [EC:6.3.5.1] [DE:PROTEIN] [SP:P18843:P78235] [DB:swissprot] >pir: [LN:D64933] [AC:D64933:A26928] [PN:NAD+ synthase (glutamine-hydrolyzing),:nitrogen-regulatory protein] [GN:nadE] [CL:spore outgrowth factor B] [OR:Escherichia coli] [EC:6.3.5.1] [DB:pir2] [MP:34-39 min] >gp: [GI:d1016252:g1742846] [LN:D90817] [AC:D90817:AB001340] [PN:NH(3)-dependent NAD(+) synthetase (EC 6.3.5.1)] [GN:nadE, efg, ntrL\_] [OR:Escherichia coli] [SR:Escherichia coli (strain:K12) DNA, clone\_lib:Kohara lambda minise] [DB:genpept-bct1] [DE:E.coli genomic DNA, Kohara clone #326(39.1-39.4 min.)] [NT:ORF\_ID:o326#9; similar to [SwissProt Accession] [LE:7818] [RE:8645] [DI:direct] >gp: [GI:d1016258:g1742853] [LN:D90818] [AC:D90818:AB001340] [PN:NH(3)-dependent NAD(+) synthetase (EC 6.3.5.1)] [GN:nadE, efg, ntrL\_] [OR:Escherichia coli] [SR:Escherichia coli (strain:K12) DNA, clone\_lib:Kohara lambda minise] [DB:genpept-bct1] [DE:E.coli genomic DNA, Kohara clone #327(39.2-39.5 min.)] [NT:ORF\_ID:o326#9; similar to [SwissProt Accession] [LE:2186] [RE:3013] [DI:direct] >gp: [GI:g1788036] [LN:AE000269] [AC:AE000269:U00096] [PN:NAD synthetase, prefers NH3 over glutamine] [GN:nadE] [FN:enzyme; Biosynthesis of cofactors, carriers:] [OR:Escherichia coli] [DB:genpept-bct2] [EC:6.3.5.1] [DE:Escherichia coli K-12 MG1655 section 159 of 400 of the complete genome.] [NT:o275; residues 32-274 are 100 pct identical to] [LE:1232] [RE:2059] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000994_6147252_c1_473	2517	6289	846	281	150	1.6e-08

Description

sp: [LN:TAGG\_BACSU] [AC:P42953] [GN:TAGG] [OR:BACILLUS SUBTILIS] [DE:TEICHOIC ACID TRANSLOCATION PERMEASE PROTEIN TAGG] [SP:P42953] [DB:swissprot] >pir:[LN:S69202] [AC:S69202:H69720] [PN:teichoic acid permease tagG:integral membrane protein tagG] [GN:tagG] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:g755152] [LN:BSU13832] [AC:U13832] [PN:highly hydrophobic integral membrane protein] [GN:tagG] [FN:teichoic acid translocation] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis 168 highly hydrophobic integral membrane protein(tagG) gene and ATP-binding protein (tagH) gene, complete cds.] [LE:287] [RE:1114] [DI:direct] >gp:[GI:e1184477:g2636097] [LN:BSUB0019] [AC:Z99122:AL009126] [PN:permease] [GN:tagG] [FN:teichoic acid translocation] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.] [SP:P42953] [LE:77137] [RE:77964] [DI:complement] >gp:[GI:e1184477:g2636097] [LN:BSUB0019] [AC:Z99122:AL009126] [PN:permease] [GN:tagG] [FN:teichoic acid translocation] [OR:Bacillus subtilis] [DB:genpept] [DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.] [SP:P42953] [LE:77137] [RE:77964] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503000994_632661_c2_560	2518	6290	777	258	490	8.8e-47
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Description

gp:[GI:g3820538] [LN:AF080002] [AC:AF080002] [PN:cobyric acid synthase CobQ] [GN:cobQ] [OR:Heliobacillus mobilis] [DB:genpept-bct2] [DE:Heliobacillus mobilis exopolyphosphatase Ppx (ppx) gene, partialcds; cobyric acid synthase CobQ (cobQ), UDP-N-acetylmuramyltripeptide synthetase MurC (murC), glutamyl tRNA reductase HemA(hemA), photosynthesis gene cluster, complete sequence, stage II sporulation protein E Sp2E (sp2E), cell cycle protein MesJ (mesJ), and ATP-dependent zinc metallopeptidase FtsH (ftsH) genes, completecds; and nucleoside diphosphate kinase B NdkB (ndkB) gene, partialcds.] [LE:1238] [RE:1996] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503000994_6682627_c3_604	2519	6291	357	118	123	6.9e-08
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Description

gp:[GI:g624123] [LN:PBU42580] [AC:U42580:U17055:U32570] [GN:a58L] [OR:Paramecium bursaria Chlorella virus 1] [DB:genpept-vrl] [DE:Paramecium bursaria Chlorella virus 1, complete genome.] [NT:contains Glu-, Gln-rich regions: QVQVV (11X), KEVWE] [LE:31140] [RE:31628] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503000994_6829687_c2_512	2520	6292	618	205	355	1.8e-32
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Description

pir:[LN:S42925] [AC:S42925] [PN:probable transport protein] [CL:ATP-binding cassette homology] [OR:Staphylococcus aureus] [DB:pir2] >gp:[GI:g459256] [LN:SASTPSMP] [AC:Z30588] [PN:Potential ABC transporter] [GN:stpC] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:S.aureus (RN4220) genes for potential ABC transporter and potentialmembrane spanning protein.] [LE:199] [RE:894] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503000994_6931261_c1_409	2521	6293	537	178	128	2.0e-08
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Description

gp: [GI:g2689551] [LN:U93688] [AC:U93688] [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus toxic shock syndrome toxin-1 (tst), enterotoxin (ent), and integrase (int) genes, complete cds.] [NT:orf4] [LE:3868] [RE:4395] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503000994_7164087_c2_575	2522	6294	333	110	217	7.5e-18
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Description

pir: [LN:A69801] [AC:A69801] [PN:hypothetical protein yfhH] [GN:yfhH] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1182843:g2633177] [LN:BSUB0005] [AC:Z99108:AL009126] [GN:yfhH] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 5 of 21): from 802821 to 1011250.] [LE:123116] [RE:123430] [DI:direct] >gp: [GI:d1025390:g2804538] [LN:D85082] [AC:D85082] [PN:YfhH] [OR:Bacillus subtilis] [SR:Bacillus subtilis DNA] [DB:genpept-bct1] [DE:Bacillus subtilis DNA, genome sequence, 79 to 81 degree region.] [LE:16007] [RE:16321] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503000994_7207518_f2_267	2523	6295	375	124	151	7.4e-11
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Description

pir: [LN:B27059] [AC:B27059] [PN:hypothetical protein 2] [OR:Glycine max] [SR:, soybean] [DB:pir2]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503000994_789010_c3_620	2524	6296	132	43		
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503000994_799188_f1_118	2525	6297	468	155	252	9.8e-20
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Description

gp: [GI:g3929312] [LN:AF100426] [AC:AF100426] [PN:fimbriae-associated protein Fap1] [GN:fap1] [OR:Streptococcus parasanguinis] [DB:genpept-bct2] [DE:Streptococcus parasanguis fimbriae-associated protein Fap1 (fap1) gene, complete cds.] [NT:involved in fimbriae assembly and fimbriae-mediated] [LE:284] [RE:7996] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503000994_815903_c1_423	2526	6298	141	46		
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000994_820325_f2_156	2527	6299	948	315	1131	1.1e-114
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Description

sp: [LN:GSAB\_BACSU] [AC:P71084] [GN:GSAB] [OR:BACILLUS SUBTILIS] [EC:5.4.3.8]  
 [DE: (GLUTAMATE-1-SEMALDEHYDE AMINOTRANSFERASE) (GSA-AT)] [SP:P71084] [DB:swissprot]  
 >gp: [GI:e281581:g1673394] [LN:BSZ82044] [AC:Z82044] [PN:glutamate-1-semialdehyde  
 aminotransferase] [GN:gsaB] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B. subtilis 25  
 kb genomic DNA segment (from sspE to katA).] [SP:P71084] [LE:5984] [RE:7273]  
 [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000994_860677_f1_3	2528	6300	177	58	72	0.017
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Description

gp: [GI:g3845668] [LN:AF021254] [AC:AF021254] [PN:unknown] [GN:RTL5] [OR:avian  
 adenovirus type 8] [DB:genpept-vrl] [DE:Avian adenovirus type 8 strain ATCC A-2A 100 K  
 protein homolog, partial cds; RTL10, RTR1, late 33 K protein homolog, pVIIIhomolog,  
 RTL9, RTR2, fibre homolog, RTL8, RTL7, RTL6, RTL5, andRTR3 genes, complete cds; and  
 RTL4 gene, partial cds.] [LE:8905] [RE:9216] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000994_885756_c3_662	2529	6301	180	59		
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000994_979712_c1_430	2530	6302	1422	473	111	0.023
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Description

pir: [LN:C71610] [AC:C71610] [PN:probable membrane associated protein PFB0615c]  
 [GN:PFB0615c] [OR:Plasmodium falciparum] [DB:pir2] >gp: [GI:g3845231] [LN:AE001406]  
 [AC:AE001406:AE001362] [PN:predicted membrane associated protein] [GN:PFB0615c]  
 [OR:Plasmodium falciparum] [SR:malaria parasite P. falciparum] [DB:genpept-inv2]  
 [DE:Plasmodium falciparum chromosome 2, section 43 of 73 of thecomplete sequence.]  
 [NT:predicted by GlimmerM] [LE:1921:2496:6961] [RE:2310:6749:8358] [DI:complementJoin]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000994_985678_c3_646	2531	6303	975	324	889	4.6e-89
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Description

pir: [LN:F69795] [AC:F69795] [PN:conserved hypothetical protein yerQ] [GN:yerQ]  
 [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1182652:g2632986] [LN:BSUB0004]  
 [AC:Z99107:AL009126] [GN:yerQ] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1]  
 [DE:Bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.]  
 [NT:similar to hypothetical proteins] [LE:135242] [RE:136153] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000994_9859433_c2_561	2532	6304	126	41		
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000995_10580443_c1_140	2533	6305	237	78	246	6.4e-21

Description

sp: [LN:YEED\_ECOLI] [AC:P33014] [GN:YEED] [OR:ESCHERICHIA COLI] [DE:HYPOTHETICAL 8.1 KD PROTEIN IN SBCB-HISL INTERGENIC REGION] [SP:P33014] [DB:swissprot] >pir: [LN:C64966] [AC:C64966] [PN:yeeD protein] [GN:yeeD] [CL:conserved hypothetical protein HI0721] [OR:Escherichia coli] [DB:pir2] >gp: [GI:d1016564:g1736686] [LN:D90839] [AC:D90839:AB001340] [GN:yeeD] [OR:Escherichia coli] [SR:Escherichia coli (strain:K12) DNA, clone\_lib:Kohara lambda minise] [DB:genpept-bct1] [DE:E.coli genomic DNA, Kohara clone #349(44.6-45.0 min.)] [NT:ORF\_ID:o349#3; similar to [SwissProt Accession] [LE:12878] [RE:13105] [DI:complement] >gp: [GI:d1016569:g1736692] [LN:D90840] [AC:D90840:AB001340] [GN:yeeD] [OR:Escherichia coli] [SR:Escherichia coli (strain:K12) DNA, clone\_lib:Kohara lambda minise] [DB:genpept-bct1] [DE:E.coli genomic DNA, Kohara clone #350(44.9-45.2 min.)] [NT:ORF\_ID:o349#3; similar to [SwissProt Accession] [LE:1569] [RE:1796] [DI:complement] >gp: [GI:g405955] [LN:ECOHU43] [AC:U00009] [PN:yeeD] [OR:Escherichia coli] [SR:Escherichia coli K12 BHB2600] [DB:genpept-bct1] [DE:sbcB region of E.coli K12 BHB2600.] [NT:similar to ORF in fliE-amyA intergenic region] [LE:4083] [RE:4310] [DI:complement] >gp: [GI:g1788322] [LN:AE000292] [AC:AE000292:U00096] [PN:orf, hypothetical protein] [GN:yeeD] [FN:orf; Unknown] [OR:Escherichia coli] [DB:genpept-bct2] [DE:Escherichia coli K-12 MG1655 section 182 of 400 of the complete genome.] [NT:f75; 100 pct identical to YEED\_ECOLI SW: P33014] [LE:9541] [RE:9768] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000995_12142768_f1_32	2534	6306	300	99	110	4.2e-06

Description

pir: [LN:D71245] [AC:D71245] [PN:hypothetical protein PH0221] [GN:PH0221] [OR:Pyrococcus horikoshii] [DB:pir2] >gp: [GI:d1030234:g3256608] [LN:AP000001] [AC:AP000001:AB009465:AB009464:AB009466:AB009467:AB009468:AB009469] [PN:235aa long hypothetical protein] [GN:PH0221] [OR:Pyrococcus horikoshii] [SR:Pyrococcus horikoshii (strain:OT3) DNA] [DB:genpept-bct1] [DE:Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt. position (1/7).] [LE:194212] [RE:194919] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000995_13907566_c1_148	2535	6307	144	47		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000995_14493812_c1_131	2536	6308	465	154	289	1.8e-25

Description

pir: [LN:C69786] [AC:C69786] [PN:conserved hypothetical protein ydiB] [GN:ydiB] [CL:hypothetical protein HI0065] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1182570:g2632904] [LN:BSUB0004] [AC:Z99107:AL009126] [GN:ydiB] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 4 of 21): from 600701 to 813890.] [NT:similar to hypothetical proteins] [LE:40670] [RE:41146] [DI:direct] >gp: [GI:d1020494:g1945107] [LN:D88802] [AC:D88802] [GN:ydiB] [OR:Bacillus subtilis] [SR:Bacillus subtilis (sub\_species:Marburg, strain:168, isolate:JH642) [DB:genpept-bct1] [DE:Bacillus subtilis DNA for phoB-rrnE-groESL region, complete cds.] [NT:E. coli hypothetical protein; P31805 (267)] [LE:27672] [RE:28148] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000995_1461637_f2_60	2537	6309	249	82	123	6.9e-08

Description

sp: [LN:ILVN\_BACSU] [AC:P37252] [GN:ILVN] [OR:BACILLUS SUBTILIS] [EC:4.1.3.18] [DE:(ACETOHYDROXY-ACID SYNTHASE SMALL SUBUNIT) (ALS)] [SP:P37252] [DB:swissprot] >pir: [LN:E69644] [AC:E69644] [PN:acetolactate synthase (small subunit) ilvN] [GN:ilvN] [CL:acetolactate synthase small chain] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:g143092] [LN:BACILNB] [AC:L03181] [PN:acetolactate synthase small subunit] [GN:ilvN] [OR:Bacillus subtilis] [SR:Bacillus subtilis DNA] [DB:genpept-bct1] [DE:Bacillus subtilis ilvB, ilvN and ilvC genes, complete ilv-leuoperon.] [LE:2438] [RE:2962] [DI:direct] >gp: [GI:e1184079:g2635295] [LN:BSUB0015] [AC:Z99118:AL009126] [PN:acetolactate synthase (acetohydroxy-acid) [GN:ilvN] [FN:valine/isoleucine biosynthesis] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:4.1.3.18] [DE:Bacillus subtilis complete genome (section 15 of 21): from 2795131 to 3013540.] [SP:P37252] [LE:98696] [RE:99220] [DI:complement] >gp: [GI:e1165365:g1770067] [LN:BSZ75208] [AC:Z75208] [PN:acetolactate synthase small subunit] [GN:ilvN] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:4.1.3.18] [DE:B. subtilis genomic sequence 89009bp.] [NT:acetolactate synthase (acetohydroxy-acid synthase)] [SP:P37252] [LE:70687] [RE:71211] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000995_14849093_c3_180	2538	6310	294	97	133	6.0e-09

Description

pir: [LN:F71245] [AC:F71245] [PN:hypothetical protein PHS004] [GN:PHS004] [OR:Pyrococcus horikoshii] [DB:pir2] >gp: [GI:d1030236:g3256610] [LN:AP000001] [AC:AP000001:AB009465:AB009464:AB009466:AB009467:AB009468:AB009469] [PN:58aa long hypothetical protein] [GN:PHS004] [OR:Pyrococcus horikoshii] [SR:Pyrococcus horikoshii (strain:OT3) DNA] [DB:genpept-bct1] [DE:Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt. position (1/7).] [NT:similar to GENPEPT:Z47547 percent identity:50.000] [LE:195255] [RE:195431] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000995_14897837_f1_29	2539	6311	1275	424	1161	4.3e-128

Description

sp: [LN:THD1\_LACLA] [AC:Q02145] [GN:ILVA] [OR:LACTOCOCCUS LACTIS] [SR:, SUBSPLACTIS:STREPTOCOCCUS LACTIS] [EC:4.2.1.16] [DE:DEAMINASE] [SP:Q02145] [DB:swissprot] >pir: [LN:S35141] [AC:S35141] [PN:probable threonine dehydratase,] [GN:ilvA] [CL:threonine dehydratase] [OR:Lactococcus lactis subsp. lactis] [EC:4.2.1.16] [DB:pir2]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000995_157802_c1_135	2540	6312	141	46		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000995_1702_f2_36	2541	6313	522	173	88	0.0089

Description

pir: [LN:T00168] [AC:T00168] [PN:hypothetical protein 33] [OR:Staphylococcus aureus phage phi PVL] [DB:pir3] >gp: [GI:d1032869:g3341942] [LN:AB009866] [AC:AB009866] [OR:bacteriophage phi PVL] [SR:bacteriophage phi PVL (specific\_host:Staphylococcus aureus ATC) [DB:genpept-phg] [DE:Bacteriophage phi PVL proviral DNA, complete sequence.] [NT:orf 33] [LE:28172] [RE:28582] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000995_19564128_c2_172	2542	6314	315	104		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000995_20422318_f3_73	2543	6315	417	138	105	2.2e-05

Description

pir:[LN:D69633] [AC:D69633] [PN:glutamine ABC transporter (glutamine-binding protein) glnH] [GN:glnH] [CL:lysine-arginine-ornithine-binding protein] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1183973:g2635189] [LN:BSUB0014] [AC:Z99117:AL009126] [PN:glutamine ABC transporter (glutamine-binding) [GN:glnH] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 14 of 21): from 2599451 to 2812870.] [LE:202928] [RE:203749] [DI:direct] >gp:[GI:e1183991:g2635207] [LN:BSUB0015] [AC:Z99118:AL009126] [PN:glutamine ABC transporter (glutamine-binding) [GN:glnH] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 15 of 21): from 2795131 to 3013540.] [LE:7248] [RE:8069] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000995_2114077_c2_166	2544	6316	156	51	115	1.1e-06

Description

pir:[LN:D69786] [AC:D69786] [PN:glycoprotein endopeptidase homolog ydiC] [GN:ydiC] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1182571:g2632905] [LN:BSUB0004] [AC:Z99107:AL009126] [GN:ydiC] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 4 of 21): from 600701 to 813890.] [NT:similar to glycoprotein endopeptidase] [LE:41127] [RE:41816] [DI:direct] >gp:[GI:d1020495:g1945108] [LN:D88802] [AC:D88802] [GN:ydiC] [OR:Bacillus subtilis] [SR:Bacillus subtilis (sub\_species:Marburg, strain:168, isolate:JH642] [DB:genpept-bct1] [DE:Bacillus subtilis DNA for phoB-rrnE-groESL region, complete cds.] [NT:H. influenzae hypothetical protein; P43990 (182)] [LE:28129] [RE:28818] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000995_2125637_f3_111	2545	6317	150	49		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000995_22441907_f2_58	2546	6318	1869	622	1924	9.7e-199

Description

sp:[LN:ILVD\_BACSU] [AC:P51785] [GN:ILVD] [OR:BACILLUS SUBTILIS] [EC:4.2.1.9] [DE:110] (VEG110) [SP:P51785] [DB:swissprot]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000995_22766502_f1_18	2547	6319	135	44		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000995_23478463_f3_99	2548	6320	1755	584	1667	1.7e-171

Description

pir: [LN:B69644] [AC:B69644:I39865] [PN:acetolactate synthase, large chain] [GN:ilvB] [CL:acetolactate synthase large chain:thiamine pyrophosphate-binding domain homology] [OR:Bacillus subtilis] [EC:4.1.3.18] [DB:pir2] >gp: [GI:e1184080:g2635296] [LN:BSUB0015] [AC:Z99118:AL009126] [PN:acetolactate synthase (acetohydroxy-acid) [GN:ilvB] [FN:valine/isoleucine biosynthesis] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:4.1.3.18] [DE:Bacillus subtilis complete genome (section 15 of 21): from 2795131 to 3013540.] [LE:99217] [RE:100941] [DI:complement] >gp: [GI:e1165364:g1770066] [LN:BSZ75208] [AC:Z75208] [PN:acetolactate synthase large subunit] [GN:ilvB] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:4.1.3.18] [DE:B. subtilis genomic sequence 89009bp.] [NT:acetolactate synthase (acetohydroxy-acid synthase)] [LE:68966] [RE:70690] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000995_23867325_f2_64	2549	6321	570	189	561	2.6e-54

Description

sp: [LN:LEUD\_LACLA] [AC:Q02144] [GN:LEUD] [OR:LACTOCOCCUS LACTIS] [SR:,SUBSPLACTIS:STREPTOCOCCUS LACTIS] [EC:4.2.1.33] [DE:(ISOPROPYLMALATE ISOMERASE) (ALPHA-IPM ISOMERASE)] [SP:Q02144] [DB:swissprot] >pir: [LN:E36889] [AC:E36889:S35135] [PN:probable 3-isopropylmalate dehydratase, chain leuD] [GN:leuD] [CL:3-isopropylmalate dehydratase small chain] [OR:Lactococcus lactis subsp. lactis] [EC:4.2.1.33] [DB:pir2] >gp: [GI:g2565154] [LN:LLU92974] [AC:U92974:M90760:M90761] [PN:LeuD] [GN:leuD] [OR:Lactococcus lactis] [DB:genpept-bct1] [DE:Lactococcus lactis unknown gene, partial cds, and HisC (hisC), unknown, HisG (hisG), unknown, HisB (hisB), unknown, HisH (hish), HisA (hisA), HisF (hisF), HisIE (hisIE), unknown, unknown, LeuA (leuA), LeuB (leuB), LeuC (leuC), LeuD (leuD), unknown, IlvD (ilvD), IlvB (ilvB), IlvN, IlvC (ilvC), IlvA (ilvA), AldB (aldb) and aldR (aldR) genes, complete cds.] [NT:isopropylmalate dehydratase subunit] [LE:16590] [RE:17165] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000995_24343813_c1_139	2550	6322	1119	372	1075	9.0e-109

Description

sp: [LN:YEEE\_ECOLI] [AC:P33015] [GN:YEEE] [OR:ESCHERICHIA COLI] [DE:HYPOTHETICAL 38.1 KD PROTEIN IN SBCB-HISL INTERGENIC REGION] [SP:P33015] [DB:swissprot] >pir: [LN:D64966] [AC:D64966] [PN:membrane protein yeeE] [GN:yeeE] [OR:Escherichia coli] [DB:pir2] >gp: [GI:d1016565:g1736687] [LN:D90839] [AC:D90839:AB001340] [GN:yeeE] [OR:Escherichia coli] [SR:Escherichia coli (strain:K12) DNA, clone\_lib:Kohara lambda minise] [DB:genpept-bct1] [DE:E.coli genomic DNA, Kohara clone #349(44.6-45.0 min.)] [NT:ORF\_ID:o349#4; similar to [SwissProt Accession] [LE:13119] [RE:14177] [DI:complement] >gp: [GI:d1016570:g1736693] [LN:D90840] [AC:D90840:AB001340] [GN:yeeE] [OR:Escherichia coli] [SR:Escherichia coli (strain:K12) DNA, clone\_lib:Kohara lambda minise] [DB:genpept-bct1] [DE:E.coli genomic DNA, Kohara clone #350(44.9-45.2 min.)] [NT:ORF\_ID:o349#4; similar to [SwissProt Accession] [LE:1810] [RE:2868] [DI:complement] >gp: [GI:g405956] [LN:ECOHU43] [AC:U00009] [PN:yeeE] [OR:Escherichia coli] [SR:Escherichia coli K12 BHB2600] [DB:genpept-bct1] [DE:sbcB region of E.coli K12 BHB2600.] [NT:similar to ORF in fliE-amyA intergenic region] [LE:4324] [RE:5382] [DI:complement] >gp: [GI:g1788323] [LN:AE000292] [AC:AE000292:U00096] [PN:putative transport system permease protein] [GN:yeeE] [FN:putative transport; Not classified] [OR:Escherichia coli] [DB:genpept-bct2] [DE:Escherichia coli K-12 MG1655 section 182 of 400 of the complete genome.] [NT:f352; 100 pct identical to YEEE\_ECOLI SW: P33015] [LE:9782] [RE:10840] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000995_24640625_c2_175	2551	6323	960	319	954	6.0e-96

Description

sp: [LN:SCRR\_STAXY] [AC:P74892] [GN:SCRR] [OR:STAPHYLOCOCCUS XYLOSUS] [DE:SUCROSE OPERON REPRESSOR (SCR OPERON REGULATORY PROTEIN)] [SP:P74892] [DB:swissprot]  
 >gp: [GI:e264641:g949974] [LN:SXSCRBA] [AC:X67744] [PN:sucrose repressor] [GN:scrR] [OR:Staphylococcus xylosus] [DB:genpept-bct1] [DE:S.xylosus scrB and scrR genes.] [SP:P74892] [LE:495] [RE:1457] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000995_24646962_c1_150	2552	6324	210	69	79	0.0032

Description

gp: [GI:g2564351] [LN:VCU83795] [AC:U83795] [PN:RstR] [GN:rstR] [FN:repressor of rstA transcription] [OR:Vibrio cholerae] [DB:genpept-bct1] [DE:Vibrio cholerae RstR (rstR), RstA1 (rstA1), RstB1 (rstB1) and RstC(rstC) genes, complete cds.] [LE:496] [RE:834] [DI:complement] >gp: [GI:g2564356] [LN:VCU83796] [AC:U83796] [PN:RstR] [GN:rstR] [FN:repressor of rstA transcription] [OR:Vibrio cholerae] [DB:genpept-bct1] [DE:Vibrio cholerae RstR (rstR), RstA2 (rstA2), and RstB2 (rstB2)genes, complete cds.] [LE:496] [RE:834] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000995_24814812_f3_90	2553	6325	1950	649	1516	1.7e-155

Description

sp: [LN:YDIF\_BACSU] [AC:O05519] [GN:YDIF] [OR:BACILLUS SUBTILIS] [DE:HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YDIF] [SP:O05519] [DB:swissprot] >pir: [LN:G69786] [AC:G69786] [PN:ABC transporter (ATP-binding protein) homolog ydiF] [GN:ydiF] [CL:ATP-binding cassette homology] [OR:Bacillus subtilis] [DB:pir2]  
 >gp: [GI:e1182574:g2632908] [LN:BSUB0004] [AC:Z99107:AL009126] [GN:ydiF] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 4 of 21): from 600701 to 813890.] [NT:similar to ABC transporter (ATP-binding protein)] [SP:O05519] [LE:43544] [RE:45472] [DI:complement] >gp: [GI:d1020498:g1945111] [LN:D88802] [AC:D88802] [GN:ydiF] [OR:Bacillus subtilis] [SR:Bacillus subtilis (sub\_species:Marburg, strain:168, isolate:JH642) [DB:genpept-bct1] [DE:Bacillus subtilis DNA for phoB-rrnE-groESL region, complete cds.] [NT:H. influenzae hypothetical ABC transporter; P44808] [LE:30546] [RE:32474] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000995_24823588_f2_63	2554	6326	1386	461	1633	6.7e-168

Description

sp: [LN:LEU2\_LACLA] [AC:Q02142] [GN:LEUC] [OR:LACTOCOCCUS LACTIS] [SR:,SUBSPLACTIS:STREPTOCOCCUS LACTIS] [EC:4.2.1.33] [DE:(ISOPROPYLMALATE ISOMERASE) (ALPHA-IPM ISOMERASE) (IPMI)] [SP:Q02142] [DB:swissprot] >pir: [LN:S35134] [AC:S35134] [PN:probable 3-isopropylmalate dehydratase, chain leuC] [GN:leuC] [OR:Lactococcus lactis subsp. lactis] [SR:strain NCDO2118, , strain NCDO2118] [SR:strain NCDO2118, ] [EC:4.2.1.33] [DB:pir2] >gp: [GI:g2565153] [LN:LLU92974] [AC:U92974:M90760:M90761] [PN:LeuC] [GN:leuC] [OR:Lactococcus lactis] [DB:genpept-bct1] [DE:Lactococcus lactis unknown gene, partial cds, and HisC (hisC), unknown, HisG (hisG), unknown, HisB (hisB), unknown, HisH (hish), HisA (hisA), HisF (hisF), HisIE (hisIE), unknown, unknown, LeuC (leuC), LeuB (leuB), LeuC (leuC), LeuD (leuD), unknown, IlvD (ilvD), IlvB (ilvB), IlvN, IlvC (ilvC), IlvA (ilvA), AldB (aldb) and aldB (aldB) genes, complete cds.] [NT:isopropylmalate dehydratase subunit] [LE:15188] [RE:16570] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000995_25900300_c3_212	2555	6327	330	110	297	2.5e-26

Description

gp: [GI:g2689561] [LN:U93688] [AC:U93688] [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus toxic shock syndrome toxin-1 (tst), enterotoxin (ent), and integrase (int) genes, complete cds.] [NT:orf14] [LE:10769] [RE:11029] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503000995_26615912_c3_206	2556	6328	1479	492	1943	9.5e-201
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Description

sp: [LN:SCRB\_STAXY] [AC:Q05936] [GN:SCRB] [OR:STAPHYLOCOCCUS XYLOSUS] [EC:3.2.1.26] [DE:SUCROSE-6-PHOSPHATE HYDROLASE, (SUCRASE) (INVERTASE)] [SP:Q05936] [DB:swissprot] >pir: [LN:A47059] [AC:A47059] [PN:sucrase ScrB] [OR:Staphylococcus xylosus] [DB:pir2] >gp: [GI:e264653:g288269] [LN:SXSCRBA] [AC:X67744] [PN:beta-fructofuranosidase] [GN:scrB] [OR:Staphylococcus xylosus] [DB:genpept-bct1] [EC:3.2.1.26] [DE:S.xylosus scrB and scrR genes.] [SP:Q05936] [LE:1541] [RE:3025] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503000995_2866090_f2_35	2557	6329	1254	417	1250	2.6e-127
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Description

gp: [GI:g2689564] [LN:U93688] [AC:U93688] [PN:integrase] [GN:int] [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus toxic shock syndrome toxin-1 (tst), enterotoxin (ent), and integrase (int) genes, complete cds.] [NT:similar to staphylococcal phage integrase] [LE:13871] [RE:15091] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503000995_29307312_c3_181	2558	6330	165	54		
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503000995_31436_f1_15	2559	6331	177	58		
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503000995_31680342_f3_74	2560	6332	546	181	176	4.6e-12
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Description

gp: [GI:g1633572] [LN:KSU52064] [AC:U52064] [OR:Kaposi's sarcoma-associated herpesvirus] [SR:Kaposi's sarcoma-associated herpesvirus - Human herpesvirus 8] [DB:genpept-vrl] [DE:Kaposi's sarcoma-associated herpes-like virus ORF73 homolog gene, complete cds.] [NT:Herpesvirus saimiri ORF73 homolog] [LE:1] [RE:3489] [DI:direct] >gp: [GI:g1718329] [LN:KSU75698] [AC:U75698] [OR:Kaposi's sarcoma-associated herpesvirus] [SR:Kaposi's sarcoma-associated herpesvirus - Human herpesvirus 8] [DB:genpept-vrl] [DE:Kaposi's sarcoma-associated herpesvirus long unique region, 80putative ORF's and kaposin gene, complete cds.] [NT:ORF 73; extensive acidic domains, potential leucine] [LE:123809] [RE:127297] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000995_33203138_c1_133	2561	6333	159	52		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000995_3361326_c2_151	2562	6334	207	68		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000995_34257878_f2_62	2563	6335	1065	354	894	1.4e-89

Description

sp: [LN:LEU3\_LACLA] [AC:Q02143] [GN:LEUB] [OR:LACTOCOCCUS LACTIS]  
 [SR:,SUBSPLACTIS:STREPTOCOCCUS LACTIS] [EC:1.1.1.85] [DE:(IMDH) (3-IPM-DH)] [SP:Q02143]  
 [DB:swissprot] >pir: [LN:S35133] [AC:S35133:C36889] [PN:3-isopropylmalate  
 dehydrogenase,] [GN:leuB] [CL:3-isopropylmalate dehydrogenase] [OR:Lactococcus lactis  
 subsp. lactis] [SR:strain NCDO2118, , strain NCDO2118] [SR:strain NCDO2118, ]  
 [EC:1.1.1.85] [DB:pir2] >gp: [GI:g2565152] [LN:LLU92974] [AC:U92974:M90760:M90761]  
 [PN:LeuB] [GN:leuB] [OR:Lactococcus lactis] [DB:genpept-bct1] [DE:Lactococcus lactis  
 unknown gene, partial cds, and HisC (hisC), unknown, HisG (hisG), unknown, HisB (hisB),  
 unknown, HisH (hish), HisA (hisA), HisF (hisF), HisIE (hisIE), unknown, unknown,  
 LeuA (leuA), LeuB (leuB), LeuC (leuC), LeuD (leuD), unknown, IlvD (ilvD), IlvB (ilvB),  
 IlvN, IlvC (ilvC), IlvA (ilvA), AldB (aldb) and aldR (aldR) genes, complete cds.]  
 [NT:isopropylmalate dehydrogenase] [LE:13788] [RE:14825] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000995_34412750_c3_207	2564	6336	966	321	1031	4.2e-104

Description

pir: [LN:S20799] [AC:S58482:S20799] [PN:hypothetical protein 7] [CL:ribokinase]  
 [OR:Staphylococcus aureus] [DB:pir2] >gp: [GI:g46512] [LN:SAAGRAB] [AC:X52543:M32737]  
 [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:S.aureus agrA, agrB and hld genes.]  
 [NT:orf 7] [LE:4896] [RE:5855] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000995_35598750_f3_72	2565	6337	849	282	112	3.9e-06

Description

gp: [GI:g2897106] [LN:AF020798] [AC:AF020798] [PN:repressor] [OR:Streptococcus  
 thermophilus bacteriophage TP-J34] [DB:genpept-phg] [DE:Streptococcus thermophilus  
 bacteriophage lysogeny module, integrasehomolog (int), putative host cell  
 surface-exposed lipoprotein,putative metallo-proteinase, repressor, Cro-like  
 regulatoryprotein, and P1-antirepressor homolog genes, complete cds.] [NT:CI-like  
 regulatory protein; orf121] [LE:4825] [RE:5190] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503000995_36132937_f2_53	2566	6338	1641	546	273	9.6e-20
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Description

sp: [LN:HEXA\_STRPN] [AC:P10564] [GN:HEXA] [OR:STREPTOCOCCUS PNEUMONIAE] [DE:DNA MISMATCH REPAIR PROTEIN HEXA] [SP:P10564] [DB:swissprot] >pir:[LN:C28667] [AC:C28667] [PN:DNA mismatch repair protein hexA] [GN:hexA] [CL:DNA mismatch repair protein mutS] [OR:Streptococcus pneumoniae] [DB:pir2] >gp:[GI:g153655] [LN:STRHEXA] [AC:M18729] [PN:mismatch repair protein] [GN:hexA] [OR:Streptococcus pneumoniae] [SR:Streptococcus pneumoniae (strain 175) (clone: pLS141.) DNA] [DB:genpept-bct1] [DE:S.pneumoniae mismatch repair protein (hexA) gene, complete cds.] [LE:971] [RE:3505] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503000995_36206502_c3_197	2567	6339	483	160	340	7.0e-31
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Description

pir:[LN:E69786] [AC:E69786] [PN:ribosomal-protein-alanine N-acetyltransfer homolog ydiD] [GN:ydiD] [CL:Escherichia coli peptide N-acetyltransferase rimI] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1182572:g2632906] [LN:BSUB0004] [AC:Z99107:AL009126] [GN:ydiD] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 4 of 21): from 600701 to 813890.] [NT:similar to ribosomal-protein-alanine] [LE:41826] [RE:42281] [DI:direct] >gp:[GI:d1020496:g1945109] [LN:D88802] [AC:D88802] [GN:ydiD] [OR:Bacillus subtilis] [SR:Bacillus subtilis (sub\_species:Marburg, strain:168, isolate:JH642] [DB:genpept-bct1] [DE:Bacillus subtilis DNA for phoB-rrnE-groESL region, complete cds.] [NT:H. influenzae, ribosomal protein alanine] [LE:28828] [RE:29283] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503000995_409556_f1_33	2568	6340	135	44	112	2.5e-06
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Description

pir:[LN:D71245] [AC:D71245] [PN:hypothetical protein PH0221] [GN:PH0221] [OR:Pyrococcus horikoshii] [DB:pir2] >gp:[GI:d1030234:g3256608] [LN:AP000001] [AC:AP000001:AB009465:AB009464:AB009466:AB009467:AB009468:AB009469] [PN:235aa long hypothetical protein] [GN:PH0221] [OR:Pyrococcus horikoshii] [SR:Pyrococcus horikoshii (strain:OT3) DNA] [DB:genpept-bct1] [DE:Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt. position (1/7).] [LE:194212] [RE:194919] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000995_4707506_c2_174	2569	6341	1314	437	1156	2.4e-117

Description

sp: [LN:NRGA\_BACSU] [AC:Q07429] [GN:NRGA] [OR:BACILLUS SUBTILIS] [DE:PROBABLE AMMONIUM TRANSPORTER (MEMBRANE PROTEIN NRGA)] [SP:Q07429] [DB:swissprot] >pir:[LN:A36865] [AC:A36865:D69667] [PN:ammonium transporter nrgA] [GN:nrgA] [CL:ammonium transporter nrgA] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:g143264] [LN:BACNRGABO] [AC:L03216] [PN:membrane-associated protein] [GN:nrgA] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain 168) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis operon membrane-associated protein (nrgA), and PII-like protein (nrgB) genes, complete cds.] [NT:putative] [LE:126] [RE:1340] [DI:direct] >gp:[GI:e1184557:g2636176] [LN:BSUB0019] [AC:Z99122:AL009126] [PN:ammonium transporter] [GN:nrgA] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091 to 3809700.] [SP:Q07429] [LE:158754] [RE:159968] [DI:direct] >gp:[GI:e283112:g1684645] [LN:BSZ82987] [AC:Z82987] [PN:unknown] [GN:nrgA] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B. subtilis ywo[A,B,C,D,E,F,G,H], nrg[A,B], spoIID and mb1 genes.] [SP:Q07429] [LE:1335] [RE:2549] [DI:complement] >gp:[GI:e1184557:g2636176] [LN:BSUB0019] [AC:Z99122:AL009126] [PN:ammonium transporter] [GN:nrgA] [OR:Bacillus subtilis] [DB:genpept] [DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091 to 3809700.] [SP:Q07429] [LE:158754] [RE:159968] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000995_4958387_c1_132	2570	6342	537	178	305	3.6e-27
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Description

pir: [LN:D69786] [AC:D69786] [PN:glycoprotein endopeptidase homolog ydiC] [GN:ydiC] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1182571:g2632905] [LN:BSUB0004] [AC:Z99107:AL009126] [GN:ydiC] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 4 of 21): from 600701 to 813890.] [NT:similar to glycoprotein endopeptidase] [LE:41127] [RE:41816] [DI:direct] >gp:[GI:d1020495:g1945108] [LN:D88802] [AC:D88802] [GN:ydiC] [OR:Bacillus subtilis] [SR:Bacillus subtilis (sub\_species:Marburg, strain:168, isolate:JH642) [DB:genpept-bct1] [DE:Bacillus subtilis DNA for phoB-rrnE-groESL region, complete cds.] [NT:H. influenzae hypothetical protein; P43990 (182)] [LE:28129] [RE:28818] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000995_5359438_c2_167	2571	6343	1107	368	1096	5.4e-111
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Description

sp: [LN:YDIE\_BACSU] [AC:O05518] [GN:YDIE] [OR:BACILLUS SUBTILIS] [DE:HYPOTHETICAL 36.8 KD PROTEIN IN PHOB-GROES INTERGENIC REGION] [SP:O05518] [DB:swissprot] >pir:[LN:F69786] [AC:F69786] [PN:glycoprotein endopeptidase homolog ydiE] [GN:ydiE] [CL:O-sialoglycoprotein endopeptidase] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1182573:g2632907] [LN:BSUB0004] [AC:Z99107:AL009126] [GN:ydiE] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 4 of 21): from 600701 to 813890.] [NT:similar to glycoprotein endopeptidase] [SP:O05518] [LE:42274] [RE:43314] [DI:direct] >gp:[GI:d1020497:g1945110] [LN:D88802] [AC:D88802] [GN:ydiE] [OR:Bacillus subtilis] [SR:Bacillus subtilis (sub\_species:Marburg, strain:168, isolate:JH642) [DB:genpept-bct1] [DE:Bacillus subtilis DNA for phoB-rrnE-groESL region, complete cds.] [NT:P. haemolytica O-sialoglycoprotein endopeptidase;] [LE:29276] [RE:30316] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503000995_5909428_c3_203	2572	6344	750	249	582	1.6e-56
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Description

gp: [GI:d1039124:g4514349] [LN:AB013375] [AC:AB013375] [PN:YdiH] [GN:ydiH] [OR:Bacillus halodurans] [SR:Bacillus halodurans (strain:C-125) DNA] [DB:genpept-bct1] [DE:Bacillus halodurans C-125 ydiH, ydiI, ydij, yhcA and yxaA genes, complete and partial cds.] [LE:235] [RE:870] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503000995_6836010_c2_153	2573	6345	171	56		
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503000995_860790_f3_101	2574	6346	1593	530	1391	3.0e-142
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Description

sp: [LN:LEU1\_LACLA] [AC:Q02141] [GN:LEUA] [OR:LACTOCOCCUS LACTIS] [SR:, SUBSPLACTIS:STREPTOCOCCUS LACTIS] [EC:4.1.3.12] [DE:SYNTHASE) (ALPHA-IPM SYNTHETASE)] [SP:Q02141] [DB:swissprot] >pir: [LN:S35132] [AC:S35132:B36889] [PN:2-isopropylmalate synthase, :alpha-isopropylmalate synthase] [GN:leuA] [CL:2-isopropylmalate synthase leuA] [OR:Lactococcus lactis subsp. lactis] [EC:4.1.3.12] [DB:pir2]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503000995_9843800_f1_8	2575	6347	192	63	47	0.020
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Description

gp: [GI:e236301:g1263146] [LN:MTMCECYTB] [AC:Z70776] [PN:cytochrome b] [OR:Mitochondrion Mugil cephalus] [SR:Mugil cephalus] [DB:genpept-vrt] [DE:M.cephalus mitochondrial cytochrome b gene.] [LE:<1] [RE:>292] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503000995_995451_f2_61	2576	6348	1020	339	1139	1.5e-115
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Description

sp: [LN:ILVC\_BACSU] [AC:P37253] [GN:ILVC] [OR:BACILLUS SUBTILIS] [EC:1.1.1.86] [DE:ISOMEROREDUCTASE) (ALPHA-KETO-BETA-HYDROXYLACIL REDUCTOISOMERASE)] [SP:P37253] [DB:swissprot] >pir: [LN:C69644] [AC:C69644] [PN:ketol-acid reductoisomerase ilvC] [GN:ilvC] [CL:Methanococcus ketol-acid reductoisomerase: ketol-acid reductoisomerase homology] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:g143093] [LN:BACILNB] [AC:L03181] [PN:ketol-acid reductoisomerase] [GN:ilvC] [OR:Bacillus subtilis] [SR:Bacillus subtilis DNA] [DB:genpept-bct1] [DE:Bacillus subtilis ilvB, ilvN and ilvC genes, complete ilv-leuoperon.] [LE:2979] [RE:4007] [DI:direct] >gp: [GI:e1184078:g2635294] [LN:BSUB0015] [AC:Z99118:AL009126] [PN:ketol-acid reductoisomerase (acetohydroxy-acid) [GN:ilvC] [FN:valine/soleucine biosynthesis] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:1.1.1.86] [DE:Bacillus subtilis complete genome (section 15 of 21): from 2795131 to 3013540.] [SP:P37253] [LE:97651] [RE:98679] [DI:complement] >gp: [GI:e1165366:g1770068] [LN:BSZ75208] [AC:Z75208] [PN:ketol-acid reductoisomerase] [GN:ilvC] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:1.1.1.86] [DE:B. subtilis genomic sequence 89009bp.] [NT:ketol-acid reductoisomerase (acetohydroxy-acid) [SP:P37253] [LE:71228] [RE:72256] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000996_10719452_c3_376	2577	6349	684	227	371	3.6e-34
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Description

sp: [LN:HLY3\_BACSU] [AC:P54175] [GN:YPLQ] [OR:BACILLUS SUBTILIS] [DE:HEMOLYSIN III HOMOLOG] [SP:P54175] [DB:swissprot] >pir:[LN:D69938] [AC:D69938] [PN:hemolysin III homolog homolog yplQ] [GN:yplQ] [CL:hemolysin III yplQ] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:g1256643] [LN:BACYACA] [AC:L77246] [GN:yplQ] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis (YAC10-9 clone) DNA region between the serA and kdg loci.] [NT:20.2% identity with NADH dehydrogenase of the] [LE:25508] [RE:26149] [DI:complement] >gp:[GI:e1183626:g2634599] [LN:BSUB0012] [AC:Z99115:AL009126] [GN:yplQ] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 12 of 21): from 2195541 to 2409220.] [NT:similar to hemolysin III homolog] [SP:P54175] [LE:99003] [RE:99644] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000996_10734567_f3_197	2578	6350	249	82		
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000996_10752342_c2_327	2579	6351	981	326	773	9.1e-77
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Description

pir: [LN:D69812] [AC:D69812] [PN:ferrichrome ABC transporter (permease) homolog yfmE] [GN:yfmE] [CL:vitamin B12 transport protein btuC] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1182740:g2633074] [LN:BSUB0005] [AC:Z99108:AL009126] [GN:yfmE] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 5 of 21): from 802821 to 1011250.] [NT:similar to ferrichrome ABC transporter (permease)] [LE:20404] [RE:21405] [DI:complement] >gp:[GI:d1023182:g2443248] [LN:D86417] [AC:D86417] [PN:YfmE] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:AC327) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis 35.7 kb genomic DNA, 70-73 degree region,complete cds.] [LE:27116] [RE:28117] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000996_10759818_c1_271	2580	6352	1008	335	669	9.5e-66
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Description

pir: [LN:B69812] [AC:B69812] [PN:ferrichrome ABC transporter (binding prote) homolog yfmC] [GN:yfmC] [CL:iron(III) dicitrate transport protein] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1182742:g2633076] [LN:BSUB0005] [AC:Z99108:AL009126] [GN:yfmC] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 5 of 21): from 802821 to 1011250.] [NT:similar to ferrichrome ABC transporter (binding)] [LE:22475] [RE:23422] [DI:complement] >gp:[GI:d1023180:g2443246] [LN:D86417] [AC:D86417] [PN:YfmC] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:AC327) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis 35.7 kb genomic DNA, 70-73 degree region,complete cds.] [LE:25099] [RE:26046] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000996_11913877_f1_49	2581	6353	123	40		
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000996_11961568_c2_311	2582	6354	945	314	1007	1.5e-101
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Description

sp: [LN:LACC\_STAAU] [AC:P11099] [GN:LACC] [OR:STAPHYLOCOCCUS AUREUS] [EC:2.7.1.144] [DE:TAGATOSE-6-PHOSPHATE KINASE, (PHOSPHOTAGATOKINASE)] [SP:P11099] [DB:swissprot] >pir: [LN:S04358] [AC:S04358] [PN:lacC protein] [GN:lacC] [CL:6-phosphofructokinase 2] [OR:Staphylococcus aureus] [DB:pir2] >gp: [GI:g46605] [LN:SALACCD] [AC:X14827] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:Staphylococcus aureus lacC and lacD genes.] [NT:lacC polypeptide (AA 1-310)] [SP:P11099] [LE:55] [RE:987] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000996_12578885_f2_109	2583	6355	366	121		
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000996_12603166_f2_89	2584	6356	303	100	110	1.6e-06
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Description

pir: [LN:G71244] [AC:G71244] [PN:hypothetical protein PH0217] [GN:PH0217] [OR:Pyrococcus horikoshii] [DB:pir2] >gp: [GI:d1030229:g3256603] [LN:AP000001] [AC:AP000001:AB009465:AB009464:AB009466:AB009467:AB009468:AB009469] [PN:106aa long hypothetical protein] [GN:PH0217] [OR:Pyrococcus horikoshii] [SR:Pyrococcus horikoshii (strain:OT3) DNA] [DB:genpept-bct1] [DE:Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt. position (1/7).] [LE:191072] [RE:191392] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000996_1287875_f3_173	2585	6357	123	40		
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000996_13680468_c2_336	2586	6358	1080	359	1133	6.4e-115
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Description

sp: [LN:YBAL\_BACSU] [AC:P50863] [GN:YBAL:REC233] [OR:BACILLUS SUBTILIS] [DE:HYPOTHETICAL 38.6 KD PROTEIN IN CWLD-GERD INTERGENIC REGION] [SP:P50863] [DB:swissprot] >pir: [LN:A69743] [AC:A69743] [PN:ATP-binding Mrp-like protein homolog ybaL] [GN:ybaL] [CL:conserved probable membrane protein YIL003w] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e95614:g1177249] [LN:BSCWLD] [AC:X74737] [GN:rec233] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis cwld, rec233 and gerD genes.] [SP:P50863] [LE:1376] [RE:2434] [DI:direct] >gp: [GI:e1182087:g2632421] [LN:BSUB0001] [AC:Z99104:AL009126] [GN:ybaL] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 1 of 21): from 1 to 213080.] [NT:alternate gene name: ybxI; similar to ATP-binding] [LE:157420] [RE:158478] [DI:direct] >gp: [GI:d1011652:g1644213] [LN:D64126] [AC:D64126] [PN:unknown] [GN:orf14] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:168) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis genes for ribosomal proteins L13 and S9, putative cell wall hydrolase CwlD, gerD protein, 16S ribosomal RNA and 23S ribosomal RNA.] [LE:6981] [RE:8039] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000996_13871068_c1_247	2587	6359	666	221	893	1.7e-89

Description

gp: [GI:d1039013:g4512410] [LN:AB017508] [AC:AB017508] [GN:rpsC] [OR:Bacillus halodurans] [SR:Bacillus halodurans (strain:C-125) DNA] [DB:genpept-bct1] [DE:Bacillus halodurans C-125 genomic DNA, 32 kb fragment, completecds.] [NT:rpsC homologue (identity of 87% to B. subtilis)] [LE:16781] [RE:17440] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000996_13886593_c2_318	2588	6360	252	83	96	5.0e-05

Description

gp: [GI:g727435] [LN:LLU23376] [AC:U23376] [OR:Lactococcus lactis] [DB:genpept-bct1] [DE:Lactococcus lactis N5-(1-carboxyethyl)-L-ornithine synthase (ceo) gene, complete cds.] [NT:putative 6-kDa protein] [LE:165] [RE:353] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000996_1408450_f2_158	2589	6361	564	187	104	9.8e-06

Description

pir: [LN:E71186] [AC:E71186] [PN:hypothetical protein PH1769] [GN:PH1769] [OR:Pyrococcus horikoshii] [DB:pir2] >gp: [GI:d1031827:g3258201] [LN:AP000007] [AC:AP000007:AB009464:AB009465:AB009521:AB009522:AB009523:AB009524] [PN:100aa long hypothetical protein] [GN:PH1769] [OR:Pyrococcus horikoshii] [SR:Pyrococcus horikoshii (strain:OT3) DNA] [DB:genpept-bct1] [DE:Pyrococcus horikoshii OT3 genomic DNA, 1485001-1738505 nt. position(7/7).] [LE:59186] [RE:59488] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000996_1410277_f1_4	2590	6362	153	50		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000996_14277217_c2_297	2591	6363	516	171	626	3.4e-61

Description

sp: [LN:RS5\_BACSU] [AC:P21467] [GN:RPSE:SPCA] [OR:BACILLUS SUBTILIS] [DE:30S RIBOSOMAL PROTEIN S5 (BS5)] [SP:P21467] [DB:swissprot] >pir: [LN:R3BS5S] [AC:D69699:S12680:S11355] [PN:ribosomal protein S5] [GN:rpsE] [CL:Escherichia coli ribosomal protein S5] [OR:Bacillus subtilis] [DB:pir1] >gp: [GI:g1044981] [LN:BACRPLP] [AC:L47971] [PN:ribosomal protein S5] [GN:rpsE] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis ribosomal protein (rplPNXEFROQ, rpmCDJ, rpsQNHEMK) genes, integral membrane protein (secY) gene, adenylatekinase (adk) gene, methionine aminopeptidase (map) gene, initiation factor 1 (infA) gene, RNA polymerase alpha (rpoA) gene.] [LE:3585] [RE:4085] [DI:direct] >gp: [GI:e1182066:g2632400] [LN:BSUB0001] [AC:Z99104:AL009126] [PN:ribosomal protein S5] [GN:rpsE] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 1 of 21): from 1 to 213080.] [SP:P21467] [LE:143359] [RE:143859] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000996_14312750_c3_354	2592	6364	492	163	665	2.5e-65

Description

sp: [LN:RL13\_STACA] [AC:Q00990] [GN:RPLM] [OR:STAPHYLOCOCCUS CARNOSUS] [DE:50S RIBOSOMAL PROTEIN L13] [SP:Q00990] [DB:swissprot] >pir: [LN:S23063] [AC:S23063] [PN:ribosomal protein L13] [GN:rplM] [CL:Escherichia coli ribosomal protein L13] [OR:Staphylococcus carnosus] [DB:pir2] >gp: [GI:g46912] [LN:SCRPLM] [AC:X63912:S79454] [PN:ribosomal protein L13] [GN:rplM] [OR:Staphylococcus carnosus] [DB:genpept-bct1] [DE:S.carnosus rplM gene for ribosomal protein L13.] [SP:Q00990] [LE:309] [RE:746] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000996_14346067_c2_316	2593	6365	1023	340	561	2.6e-54

Description

gp: [GI:g4321580] [LN:AF050114] [AC:AF050114] [PN:alginate lyase] [OR:Pseudomonas sp. W7] [DB:genpept-bct2] [DE:Pseudomonas sp. W7 alginate lyase gene, complete cds.] [LE:1] [RE:1038] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000996_14531558_f1_53	2594	6366	126	41		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000996_14900826_c3_386	2595	6367	351	116	188	8.9e-15

Description

gp: [GI:g208931] [LN:SYNORFLAC] [AC:M15619] [OR:synthetic construct] [SR:E.coli (strain SE5000) synthetic DNA, clone pKB1] [DB:genpept-syn] [DE:Synthetic E.coli ORF16/lacZ fusion protein, partial cds.] [NT:ORF16-lacZ fusion protein] [LE:29] [RE:>232] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000996_157750_c3_379	2596	6368	195	64		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000996_15879002_f2_96	2597	6369	123	40		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000996_16829627_c2_300	2598	6370	372	123	484	3.8e-46

Description

gp: [GI:g1044989] [LN:BACRPLP] [AC:L47971] [PN:ribosomal protein S13] [GN:rpsM] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis ribosomal protein (rplPNXEFROQ, rpmCDJ, rpsQNHEMK) genes, integral membrane protein (secY) gene, adenylatekinase (adk) gene, methionine aminopeptidase (map) gene, initiation factor 1 (infA) gene, RNA polymerase alpha (rpoA) gene.] [LE:8197] [RE:8562] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000996_16835333_c2_288	2599	6371	840	279	1198	8.3e-122

Description

gp: [GI:g1165306] [LN:BSU43929] [AC:U43929] [PN:L2] [GN:rplB] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis ribosomal protein gene cluster, rpsJ, rplC, rplD, rplW, rplB, rpsS, rplV and rpsC genes, complete cds, and rplP gene,partial cds.] [NT:ribosomal protein] [LE:2266] [RE:3099] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000996_197127_f2_121	2600	6372	1965	654	285	9.0e-22

Description

sp: [LN:Y4XN\_RHISN] [AC:P55706] [GN:Y4XN] [OR:RHIZOBIUM SP] [SR:NGR234,] [DE:HYPOTHETICAL 71.0 KD PROTEIN Y4XN] [SP:P55706] [DB:swissprot] >gp: [GI:g2182722] [LN:AE000106] [AC:AE000106:U00090] [PN:Y4xN] [GN:y4xN] [OR:Rhizobium sp. NGR234] [DB:genpept-bct2] [DE:Rhizobium sp. NGR234 plasmid pNGR234a, section 43 of 46 of thecomplete plasmid sequence.] [NT:hypothetical 71 kd protein; similar to Escherichia] [LE:6573] [RE:8459] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000996_19730052_c1_278	2601	6373	1479	492	990	9.2e-100

Description

pir: [LN:F69763] [AC:F69763] [PN:multidrug resistance protein homolog ycnB] [GN:ycnB] [CL:lincomycin-resistance protein lmrB] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1182351:g2632685] [LN:BSUB0003] [AC:Z99106:AL009126] [GN:ycnB] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 3 of 21): from 402751 to 611850.] [NT:similar to multidrug resistance protein] [LE:32866] [RE:34284] [DI:complement] >gp: [GI:d1009651:g1805454] [LN:D50453] [AC:D50453] [PN:homologue of multidrug resistance protein B,] [GN:ycnB] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:168 trpC2) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis DNA for 25-36 degree region containing theamyE-srfA region, complete cds.] [LE:115269] [RE:116687] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000996_19822151_c2_302	2602	6374	372	123	433	9.7e-41

Description

pir: [LN:F32307] [AC:F32307:C69696] [PN:ribosomal protein L17:ribosomal protein BL15 (rplQ)] [GN:rplQ] [CL:Escherichia coli ribosomal protein L17] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:g142464] [LN:BACALPHA] [AC:M26414] [PN:ribosomal protein L17] [GN:rplQ] [OR:Bacillus subtilis] [SR:Bacillus subtilis DNA] [DB:genpept-bct1] [DE:B.subtilis initiation factor 1, ribosomal proteins B, S13, S11, L17and RNA polymerase alpha core protein genes, complete cds.] [LE:2603] [RE:2965] [DI:direct] >gp: [GI:g1044992] [LN:BACRPLP] [AC:L47971] [PN:ribosomal protein L17] [GN:rplQ] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis ribosomal protein (rplPNXEFROQ, rpmCDJ,rpsQNHEMK) genes, integral membrane protein (secY) gene, adenylatekinase (adk) gene, methionine aminopeptidase (map) gene,initiation factor 1 (infA) gene, RNA polymerase alpha (rpoA) gene.] [LE:10177] [RE:10539] [DI:direct] >gp: [GI:e1182077:g2632411] [LN:BSUB0001] [AC:Z99104:AL009126] [PN:ribosomal protein L17 (BL15)] [GN:rplQ] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 1 of 21): from 1 to 213080.] [SP:P20277] [LE:149951] [RE:150313] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000996_20363762_c3_375	2603	6375	1215	404	587	4.7e-57

Description

gp: [GI:g5052662] [LN:AF145686] [AC:AF145686] [PN:BcDNA.LD24639] [GN:BcDNA.LD24639] [OR:Drosophila melanogaster] [SR:fruit fly] [DB:genpept-inv2] [DE:Drosophila melanogaster clone LD24639 BcDNA.LD24639 (BcDNA.LD24639)mRNA, complete cds.] [LE:199] [RE:1761] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000996_2125637_f3_165	2604	6376	150	49		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000996_21516287_f1_6	2605	6377	126	41		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000996_21751063_c1_245	2606	6378	579	192	621	1.2e-60

Description

sp: [LN:RL3\_BACST] [AC:P28600] [GN:RPLC] [OR:BACILLUS STEAROTHERMOPHILUS] [DE:50S RIBOSOMAL PROTEIN L3] [SP:P28600] [DB:swissprot] >pir: [LN:S24363] [AC:S24363:S36085] [PN:ribosomal protein L3] [GN:rpl3] [CL:Escherichia coli ribosomal protein L3] [OR:Bacillus stearothermophilus] [DB:pir2] >gp: [GI:g40102] [LN:BSRPLCLD] [AC:X67014:S42397] [PN:ribosomal protein L3] [GN:rplC] [OR:Bacillus stearothermophilus] [DB:genpept-bct1] [DE:B.stearothermophilus genes rplC and rplD for ribosomal proteins L3and L4, respectively.] [SP:P28600] [LE:52] [RE:693] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000996_21915941_c1_250	2607	6379	372	123	571	2.3e-55

Description

sp: [LN:RL14\_BACSU] [AC:P12875] [GN:RPLN] [OR:BACILLUS SUBTILIS] [DE:50S RIBOSOMAL PROTEIN L14] [SP:P12875] [DB:swissprot] >pir: [LN:R5BS4B] [AC:S05992:H69695] [PN:ribosomal protein L14] [GN:rplN] [CL:Escherichia coli ribosomal protein L14] [OR:Bacillus subtilis] [DB:pir1] >gp: [GI:g1044974] [LN:BACRPLP] [AC:L47971] [PN:ribosomal protein L14] [GN:rplN] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis ribosomal protein (rplN) gene, adenylatekinase (adk) gene, methionine aminopeptidase (map) gene,initiation factor 1 (infA) gene, RNA polymerase alpha (rpoA) gene.] [LE:675] [RE:1043] [DI:direct] >gp: [GI:g40150] [LN:BSSPC] [AC:X15664] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis S10/spc operon rpmC, rpsQ, rplN, rplX, rplE, rpsN genes.] [NT:L14 protein (AA 1-122)] [SP:P12875] [LE:840] [RE:1208] [DI:direct] >gp: [GI:e1182059:g2632393] [LN:BSUB0001] [AC:Z99104:AL009126] [PN:ribosomal protein L14] [GN:rplN] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 1 of 21): from 1 to 213080.] [SP:P12875] [LE:140449] [RE:140817] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503000996_22002318_c3_342	2608	6380	330	109	390	3.5e-36
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Description

sp: [LN:RL24\_BACST] [AC:P04455] [GN:RPLX] [OR:BACILLUS STEAROTHERMOPHILUS] [DE:50S RIBOSOMAL PROTEIN L24] [SP:P04455] [DB:swissprot] >pir:[LN:R5BS24] [AC:A02819] [PN:ribosomal protein L24] [CL:Escherichia coli ribosomal protein L24] [OR:Bacillus stearothermophilus] [DB:pir1]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503000996_22455303_f3_190	2609	6381	165	54		
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503000996_22688428_c3_383	2610	6382	144	47		
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503000996_22900877_c1_252	2611	6383	132	43		
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503000996_23460931_f2_100	2612	6384	429	142		
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503000996_23572128_c3_346	2613	6385	183	60	282	9.7e-25
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Description

sp: [LN:RL30\_STAAU] [AC:O06444] [GN:RPMD] [OR:STAPHYLOCOCCUS AUREUS] [DE:50S RIBOSOMAL PROTEIN L30] [SP:O06444] [DB:swissprot] >gp:[GI:g2078380] [LN:SAU96620] [AC:U96620] [PN:ribosomal protein L30] [GN:L30] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:Staphylococcus aureus NCTC 8325 ribosomal protein L30 (L30), ribosomal protein L15 (L15) and SecY (secY) genes, complete cds.] [LE:65] [RE:244] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000996_23572180_c3_349	2614	6386	222	73	326	2.1e-29

Description

pir: [LN:F69644] [AC:F69644] [PN:translation initiation factor IF-1] [GN:infA] [CL:translation initiation factor IF-1] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:g142459] [LN:BACALPHA] [AC:M26414] [PN:initiation factor 1] [GN:infA] [OR:Bacillus subtilis] [SR:Bacillus subtilis DNA] [DB:genpept-bct1] [DE:B. subtilis initiation factor 1, ribosomal proteins B, S13, S11, L17 and RNA polymerase alpha core protein genes, complete cds.] [LE:235] [RE:453] [DI:direct] >gp: [GI:g1044987] [LN:BACRPLP] [AC:L47971] [PN:initiation factor IF-1] [GN:infA] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis ribosomal protein (rplPNXEFROQ, rpmCDJ, rpsQNHEMK) genes, integral membrane protein (secY) gene, adenylatekinase (adk) gene, methionine aminopeptidase (map) gene, initiation factor 1 (infA) gene, RNA polymerase alpha (rpoA) gene.] [LE:7809] [RE:8027] [DI:direct] >gp: [GI:e1182072:g2632406] [LN:BSUB0001] [AC:Z99104:AL009126] [PN:initiation factor IF-1] [GN:infA] [FN:protein synthesis] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 1 of 21): from 1 to 213080.] [SP:P20458] [LE:147583] [RE:147801] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000996_23573587_c2_294	2615	6387	201	66	287	2.9e-25

Description

gp: [GI:d1039020:g4512417] [LN:AB017508] [AC:AB017508] [GN:rpsN] [OR:Bacillus halodurans] [SR:Bacillus halodurans (strain:C-125) DNA] [DB:genpept-bct1] [DE:Bacillus halodurans C-125 genomic DNA, 32 kb fragment, completecds.] [NT:rpsN homologue (identity of 92% to B. subtilis)] [LE:19712] [RE:19897] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000996_23603450_c2_317	2616	6388	585	194	85	0.0017

Description

pir: [LN:S77761] [AC:S77761] [PN:probable phosphotransferase system enzyme II, protein MC456:protein-Npi-phosphohistidine--sugar phosphotransferase] [OR:Mycoplasma capricolum] [EC:2.7.1.69] [DB:pir2]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000996_23632750_c3_365	2617	6389	525	174	726	8.7e-72

Description

pir: [LN:JC2527] [AC:JC2527:PC2381] [PN:alkaline shock protein] [GN:asp23] [OR:Staphylococcus aureus] [DB:pir2] >gp: [GI:g894289] [LN:S76213] [AC:S76213] [PN:alkaline shock protein 23] [GN:asp23] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus 912] [DB:genpept-bct1] [DE:asp23=alkaline shock protein 23 {methicillin resistant}[Staphylococcus aureus, 912, Genomic, 1360 nt].] [NT:Method: conceptual translation with partial peptide] [LE:343] [RE:852] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000996_23634813_c3_355	2618	6390	771	256	970	1.2e-97

Description

sp: [LN:LACR\_STAAU] [AC:P16644] [GN:LACR] [OR:STAPHYLOCOCCUS AUREUS] [DE:LACTOSE PHOSPHOTRANSFERASE SYSTEM REPRESSOR] [SP:P16644] [DB:swissprot] >pir: [LN:A44506] [AC:A44506] [PN:lactose operon repressor lacR] [OR:Staphylococcus aureus] [DB:pir2] >gp: [GI:g153035] [LN:STALACR] [AC:M32103] [PN:lacR repressor] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus (strain 8325-4) DNA] [DB:genpept-bct1] [DE:Staphylococcus aureus lac repressor (lacR) gene, complete cds and lacA repressor (lacA), partial cds.] [LE:1058] [RE:1813] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000996_23642761_f1_22	2619	6391	228	75	80	0.0064

Description

gp: [GI:d1000903:g220579] [LN:MUSPRIMP] [AC:D00570:J00614] [OR:Mus musculus] [SR:Mus musculus male cDNA to mRNA] [DB:genpept-rod] [DE:Mus musculus mRNA for ORFs (putative primordial protein), completecds.] [NT:open reading frame (196 AA)] [LE:584] [RE:1174] [DI:direct] >gp: [GI:d1000903:g220579] [LN:MUSPRIMP] [AC:D00570:J00614] [OR:Mus musculus] [SR:Mus musculus male cDNA to mRNA] [DB:genpept] [DE:Mus musculus mRNA for ORFs (putative primordial protein), completecds.] [NT:open reading frame (196 AA)] [LE:584] [RE:1174] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000996_23683375_c3_356	2620	6392	507	168	583	1.2e-56

Description

sp: [LN:LACA\_STRMU] [AC:P26423] [GN:LACA] [OR:STREPTOCOCCUS MUTANS] [EC:5.3.1.26] [DE:GALACTOSE-6-PHOSPHATE ISOMERASE LACA SUBUNIT,] [SP:P26423] [DB:swissprot] >pir: [LN:C43258] [AC:C43258:S27701] [PN:galactoside O-acetyltransferase,] [GN:lacA] [OR:Streptococcus mutans] [EC:2.3.1.18] [DB:pir2] >gp: [GI:g153673] [LN:STRLACOP] [AC:M80797] [PN:galactosidase acetyltransferase] [GN:lacA] [OR:Streptococcus mutans] [SR:Streptococcus mutans (strain PS14) DNA] [DB:genpept-bct1] [EC:2.3.1.18] [DE:Streptococcus mutans lac operon.] [LE:1534] [RE:1962] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000996_2379658_f2_82	2621	6393	225	74		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000996_23882135_c2_303	2622	6394	873	290	665	2.5e-65

Description

sp: [LN:YBXA\_BACSU] [AC:P40735] [GN:YBXA] [OR:BACILLUS SUBTILIS] [DE:HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YBXA] [SP:P40735] [DB:swissprot] >pir: [LN:E69751] [AC:E69751:G32307] [PN:ABC transporter (ATP-binding protein) homolog ybxA] [GN:ybxA] [CL:ATP-binding cassette homology] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1182078:g2632412] [LN:BSUB0001] [AC:Z99104:AL009126] [GN:ybxA] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 1 of 21): from 1 to 213080.] [NT:alternate gene name: ybaD; similar to ABC] [SP:P40735] [LE:150441] [RE:151286] [DI:direct] >gp: [GI:d1011641:g1644202] [LN:D64126] [AC:D64126] [PN:unknown] [GN:orf4] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:168) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis genes for ribosomal proteins L13 and S9, putative cell wall hydrolase CwlD, gerD protein, 16S ribosomal RNA and 23S ribosomal RNA.] [LE:1] [RE:846] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000996_23944052_f1_36	2623	6395	150	49		

Description

NO-HIT

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000996_24223787_c1_258	2624	6396	156	51	221	2.8e-18

Description

sp: [LN:RPOA\_BACSU] [AC:P20429] [GN:RPOA] [OR:BACILLUS SUBTILIS] [EC:2.7.7.6] [DE:ALPHA CHAIN) (RNA POLYMERASE ALPHA SUBUNIT)] [SP:P20429] [DB:swissprot] >pir: [LN:E32307] [AC:E32307:C24972:E69698] [PN:DNA-directed RNA polymerase, alpha chain rpoA:transcriptase alpha chain] [GN:rpoA] [CL:DNA-directed RNA polymerase alpha chain] [OR:Bacillus subtilis] [EC:2.7.7.6] [DB:pir2] >gp: [GI:g142463] [LN:BACALPHA] [AC:M26414] [PN:RNA polymerase alpha-core-subunit] [GN:rpoA] [OR:Bacillus subtilis] [SR:Bacillus subtilis DNA] [DB:genpept-bct1] [DE:B.subtilis initiation factor 1, ribosomal proteins B, S13, S11, L17and RNA polymerase alpha core protein genes, complete cds.] [LE:1581] [RE:2525] [DI:direct] >gp: [GI:g1044991] [LN:BACRPLP] [AC:L47971] [PN:RNA polymerase alpha-core-subunit] [GN:rpoA] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis ribosomal protein (rplPNXEFROQ, rpmCDJ, rpsQNHEMK) genes, integral membrane protein (secY) gene, adenylatekinase (adk) gene, methionine aminopeptidase (map) gene,initiation factor 1 (infA) gene, RNA polymerase alpha (rpoA) gene.] [LE:9155] [RE:10099] [DI:direct] >gp: [GI:e1182076:g2632410] [LN:BSUB0001] [AC:Z99104:AL009126] [PN:RNA polymerase (alpha subunit)] [GN:rpoA] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:2.7.7.6] [DE:Bacillus subtilis complete genome (section 1 of 21): from 1 to213080.] [SP:P20429] [LE:148929] [RE:149873] [DI:direct]

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000996_24244012_c3_374	2625	6397	546	181	280	1.6e-24

Description

pir: [LN:C70048] [AC:C70048] [PN:conserved hypothetical protein yvsG] [GN:yvsG] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1249789:g2832793] [LN:BS43KBDNA] [AC:AJ223978] [PN:YvsG protein] [GN:yvsG] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis 42.7kB DNA fragment from yvsA to yvqA.] [LE:5971] [RE:6453] [DI:complement] >gp: [GI:e1186023:g2635848] [LN:BSUB0018] [AC:Z99121:AL009126] [GN:yvsG] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.] [NT:similar to hypothetical proteins] [LE:21284] [RE:21766] [DI:direct]

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000996_24252318_c1_256	2626	6398	126	41	191	4.3e-15

Description

sp: [LN:RL36\_BACST] [AC:P07841] [GN:RPMJ] [OR:BACILLUS STEAROTHERMOPHILUS] [DE:(BL38)] [SP:P07841] [DB:swissprot] >pir: [LN:R5BS36] [AC:S08566:S59066] [PN:ribosomal protein L36:ribosomal protein BL38:ribosomal protein II] [CL:Escherichia coli ribosomal protein L36] [OR:Bacillus stearothermophilus] [DB:pir1]

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000996_24328927_f1_39	2627	6399	201	66		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000996_24337750_c2_312	2628	6400	981	326	1524	2.4e-156

Description

sp: [LN:LACD\_STAAU] [AC:P11100] [GN:LACD] [OR:STAPHYLOCOCCUS AUREUS] [EC:4.1.2.40] [DE:ALDOLASE) (D-TAGATOSE-1,6-BISPHOSPHATE ALDOLASE)] [SP:P11100] [DB:swissprot] >pir: [LN:S04359] [AC:S04359] [PN:lacD protein] [GN:lacD] [OR:Staphylococcus aureus] [DB:pir2] >gp: [GI:g46606] [LN:SALACCD] [AC:X14827] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:Staphylococcus aureus lacC and lacD genes.] [NT:lacD polypeptide (AA 1-326)] [SP:P11100] [LE:991] [RE:1971] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000996_24339718_c2_335	2629	6401	483	160	93	0.033

Description

gp: [GI:e246715:g1617437] [LN:SGCOM7865] [AC:X98110] [PN:pheromone receptor] [GN:comD2] [OR:Streptococcus gordonii] [DB:genpept-bct1] [DE:S.gordonii tRNA-Arg, comC2, comD2 & comE2 genes.] [NT:histidine kinase] [LE:656] [RE:2014] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000996_24350953_f1_10	2630	6402	132	43	72	0.017

Description

pir: [LN:G71244] [AC:G71244] [PN:hypothetical protein PH0217] [GN:PH0217] [OR:Pyrococcus horikoshii] [DB:pir2] >gp: [GI:d1030229:g3256603] [LN:AP000001] [AC:AP000001:AB009465:AB009464:AB009466:AB009467:AB009468:AB009469] [PN:106aa long hypothetical protein] [GN:PH0217] [OR:Pyrococcus horikoshii] [SR:Pyrococcus horikoshii (strain:OT3) DNA] [DB:genpept-bct1] [DE:Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt. position (1/7).] [LE:191072] [RE:191392] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000996_24397127_c2_313	2631	6403	1776	591	2460	1.5e-255

Description

sp: [LN:PTLB\_STAAU] [AC:P11162] [GN:LACE] [OR:STAPHYLOCOCCUS AUREUS] [EC:2.7.1.69] [DE:(EC 2.7.1.69) (EII-LAC)] [SP:P11162] [DB:swissprot] >pir: [LN:B28474] [AC:B28474] [PN:phosphotransferase system enzyme II,, lactose-specific, factor II] [OR:Staphylococcus aureus] [EC:2.7.1.69] [DB:pir2] >gp: [GI:g153038] [LN:STALACS] [AC:J03479:M17729] [OR:Staphylococcus aureus] [SR:S.aureus (strain 8325-4) DNA, clone pFB34] [DB:genpept-bct1] [DE:S.aureus enzyme III-lac (lacF), enzyme II-lac (lace), andphospho-beta-galactosidase (lacG) genes, complete cds.] [NT:enzyme II-lac (lacE)] [LE:413] [RE:2131] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000996_24402217_c3_350	2632	6404	405	134	560	3.4e-54

Description

sp: [LN:RS11\_BACSU] [AC:P04969] [GN:RPSK] [OR:BACILLUS SUBTILIS] [DE:30S RIBOSOMAL PROTEIN S11 (BS11)] [SP:P04969] [DB:swissprot] >pir: [LN:R3BSS1] [AC:D32307:B24972:S11361:B69700] [PN:ribosomal protein S11:ribosomal protein BS11] [GN:rpsK] [CL:Escherichia coli ribosomal protein S11] [OR:Bacillus subtilis] [DB:pir1] >gp: [GI:g142462] [LN:BACALPHA] [AC:M26414] [PN:ribosomal protein S11] [GN:rpsK] [OR:Bacillus subtilis] [SR:Bacillus subtilis DNA] [DB:genpept-bct1] [DE:B. subtilis initiation factor 1, ribosomal proteins B, S13, S11, L17 and RNA polymerase alpha core protein genes, complete cds.] [LE:1009] [RE:1404] [DI:direct] >gp: [GI:g1044990] [LN:BACRPLP] [AC:L47971] [PN:ribosomal protein S11] [GN:rpsK] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis ribosomal protein (rplPNXEFROQ, rpmCDJ, rpsQNHEMK) genes, integral membrane protein (secY) gene, adenylatekinase (adk) gene, methionine aminopeptidase (map) gene, initiation factor 1 (infA) gene, RNA polymerase alpha (rpoA) gene.] [LE:8583] [RE:8978] [DI:direct] >gp: [GI:g143451] [LN:BACRPOA] [AC:M13957] [OR:Bacillus subtilis] [SR:B. subtilis (strain 168 Marburg) DNA clone lambda-gt11-11-1] [DB:genpept-bct1] [DE:B. subtilis DNA sequence of the rpsM-rpoA interval.] [NT:ribosomal protein S11] [LE:133] [RE:528] [DI:direct] >gp: [GI:e1182075:g2632409] [LN:BSUB0001] [AC:Z99104:AL009126] [PN:ribosomal protein S11 (BS11)] [GN:rpsK] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 1 of 21): from 1 to 213080.] [SP:P04969] [LE:148357] [RE:148752] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000996_24641927_c1_273	2633	6405	1380	459	978	1.7e-98

Description

sp: [LN:YKAA\_BACFI] [AC:P30267] [OR:BACILLUS FIRMUS] [DE:HYPOTHETICAL 50.9 KD PROTEIN IN KATA 3'REGION (ORF A)] [SP:P30267] [DB:swissprot] >pir: [LN:S27491] [AC:S27491] [PN:hypothetical protein A] [OR:Bacillus firmus] [DB:pir2] >gp: [GI:g143121] [LN:BACKATA2] [AC:L02548:M74194] [OR:Bacillus firmus] [SR:Bacillus firmus DNA] [DB:genpept-bct1] [DE:B. firmus ORF A and ORF B, complete cds.] [NT:ORF A; putative] [LE:225] [RE:1616] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000996_24648312_f1_48	2634	6406	747	248	905	9.3e-91

Description

gp: [GI:g845686] [LN:STALACR] [AC:M32103] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus (strain 8325-4) DNA] [DB:genpept-bct1] [DE:Staphylococcus aureus lac repressor (lacR) gene, complete cds and lacA repressor (lacA), partial cds.] [NT:ORF-27] [LE:76] [RE:807] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000996_24744040_c1_270	2635	6407	1065	354	361	4.1e-33

Description

gp: [GI:g4982168] [LN:AE001804] [AC:AE001804:AE000512] [PN:hypothetical protein] [GN:TM1597] [OR:Thermotoga maritima] [DB:genpept-bct2] [DE:Thermotoga maritima section 116 of 136 of the complete genome.] [NT:similar to percent identity: 0.00; identified by] [LE:7299] [RE:8363] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000996_24806662_c1_248	2636	6408	237	78	252	1.5e-21

Description

sp: [LN:RL29\_BACSU] [AC:P12873] [GN:RPMC] [OR:BACILLUS SUBTILIS] [DE:50S RIBOSOMAL PROTEIN L29] [SP:P12873] [DB:swissprot] >pir: [LN:R5BS2L] [AC:S05990:E69697] [PN:ribosomal protein L29] [GN:rpmC] [CL:Escherichia coli ribosomal protein L29] [OR:Bacillus subtilis] [DB:pir1] >gp: [GI:g1044972] [LN:BACRPLP] [AC:L47971] [PN:ribosomal protein L29] [GN:rpmC] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis ribosomal protein (rplPNXEFROQ, rpmCDJ, rpsQNHEMK) genes, integral membrane protein (secY) gene, adenylatekinase (adk) gene, methionine aminopeptidase (map) gene, initiation factor 1 (infA) gene, RNA polymerase alpha (rpoA) gene.] [LE:142] [RE:342] [DI:direct] >gp: [GI:g40148] [LN:BSSPC] [AC:X15664] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B. subtilis S10/spc operon rpmC, rpsQ, rplN, rplX, rplE, rpsN genes.] [NT:L29 protein (AA 1-66)] [SP:P12873] [LE:313] [RE:513] [DI:direct] >gp: [GI:e1182057:g2632391] [LN:BSUB0001] [AC:Z99104:AL009126] [PN:ribosomal protein L29] [GN:rpmC] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 1 of 21): from 1 to 213080.] [SP:P12873] [LE:139922] [RE:140122] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000996_24855303_c3_368	2637	6409	1047	348	784	6.2e-78
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Description

pir: [LN:C69812] [AC:C69812] [PN:ferrichrome ABC transporter (permease) homolog yfmD] [GN:yfmD] [CL:ferrichrome ABC transporter] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1182741:g2633075] [LN:BSUB0005] [AC:Z99108:AL009126] [GN:yfmD] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 5 of 21): from 802821 to 1011250.] [NT:similar to ferrichrome ABC transporter (permease)] [LE:21402] [RE:22403] [DI:complement] >gp: [GI:d1023181:g2443247] [LN:D86417] [AC:D86417] [PN:YfmD] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:AC327) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis 35.7 kb genomic DNA, 70-73 degree region, complete cds.] [LE:26118] [RE:27119] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000996_25908568_c1_253	2638	6410	453	150	706	1.1e-69
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Description

sp: [LN:RL15\_STAAU] [AC:006445] [GN:RPLO] [OR:STAPHYLOCOCCUS AUREUS] [DE:50S RIBOSOMAL PROTEIN L15] [SP:006445] [DB:swissprot] >gp: [GI:g2078381] [LN:SAU96620] [AC:U96620] [PN:ribosomal protein L15] [GN:L15] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:Staphylococcus aureus NCTC 8325 ribosomal protein L30 (L30), ribosomal protein L15 (L15) and SecY (secY) genes, complete cds.] [LE:261] [RE:701] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000996_26205151_f2_85	2639	6411	156	51	123	6.9e-08
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Description

pir: [LN:B71245] [AC:B71245] [PN:hypothetical protein PH0220] [GN:PH0220] [OR:Pyrococcus horikoshii] [DB:pir2] >gp: [GI:d1030232:g3256606] [LN:AP000001] [AC:AP000001:AB009465:AB009464:AB009466:AB009467:AB009468:AB009469] [PN:171aa long hypothetical protein] [GN:PH0220] [OR:Pyrococcus horikoshii] [SR:Pyrococcus horikoshii (strain:OT3) DNA] [DB:genpept-bct1] [DE:Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt. position (1/7).] [LE:192864] [RE:193379] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000996_26360036_c3_345	2640	6412	387	128	429	2.6e-40
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Description

sp: [LN:RL18\_BACSU] [AC:P46899:P70969] [GN:RPLR] [OR:BACILLUS SUBTILIS] [DE:50S RIBOSOMAL PROTEIN L18] [SP:P46899:P70969] [DB:swissprot] >gp: [GI:g1044980] [LN:BACRPLP] [AC:L47971] [PN:ribosomal protein L18] [GN:rplR] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis ribosomal protein (rplPNXEFROQ, rpmCDJ, rpsQNHEMK) genes, integral membrane protein (secY) gene, adenylatekinase (adk) gene, methionine aminopeptidase (map) gene, initiation factor 1 (infA) gene, RNA polymerase alpha (rpoA) gene.] [LE:3198] [RE:3560] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000996_26773450_c1_249	2641	6413	285	94	380	4.0e-35
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Description

sp: [LN:RS17\_BACST] [AC:P23828] [GN:RPSQ] [OR:BACILLUS STEAROTHERMOPHILUS] [DE:30S RIBOSOMAL PROTEIN S17] [SP:P23828] [DB:swissprot] >pir: [LN:S17865] [AC:S17865:S59056] [PN:ribosomal protein S17] [GN:rps17] [CL:Escherichia coli ribosomal protein S17] [OR:Bacillus stearothermophilus] [DB:pir2]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000996_26776678_c2_290	2642	6414	372	123	431	1.6e-40
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Description

sp: [LN:RL22\_BACST] [AC:P23311] [GN:RPLV] [OR:BACILLUS STEAROTHERMOPHILUS] [DE:50S RIBOSOMAL PROTEIN L22] [SP:P23311] [DB:swissprot] >pir: [LN:S10612] [AC:S10612] [PN:ribosomal protein L22] [CL:Escherichia coli ribosomal protein L22] [OR:Bacillus stearothermophilus] [DB:pir2] >gp: [GI:g40107] [LN:BSRPLS] [AC:X54994] [PN:ribosomal protein L22] [OR:Bacillus stearothermophilus] [DB:genpept-bct1] [DE:B.stearothermophilus gene for ribosomal proteins L2, S19, L22, S3, and L16.] [SP:P23311] [LE:923] [RE:1264] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000996_2735801_c1_269	2643	6415	1848	615	274	1.3e-20
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Description

sp: [LN:Y4XN\_RHISN] [AC:P55706] [GN:Y4XN] [OR:RHIZOBIUM SP] [SR:NGR234,] [DE:HYPOTHETICAL 71.0 KD PROTEIN Y4XN] [SP:P55706] [DB:swissprot] >gp: [GI:g2182722] [LN:AE000106] [AC:AE000106:U00090] [PN:Y4XN] [GN:y4xN] [OR:Rhizobium sp. NGR234] [DB:genpept-bct2] [DE:Rhizobium sp. NGR234 plasmid pNGR234a, section 43 of 46 of thecomplete plasmid sequence.] [NT:hypothetical 71 kd protein; similar to Escherichia] [LE:6573] [RE:8459] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000996_277312_c1_276	2644	6416	1353	450	452	9.4e-43
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Description

gp: [GI:e1391039:g4467970] [LN:MXEGLBG] [AC:X76640] [PN:hypothetical protein] [FN:transmembrane protein, putative] [OR:Myxococcus xanthus] [DB:genpept-bct1] [DE:Myxococcus xanthus celA gene and ORFX.] [NT:ORFX] [LE:669] [RE:2192] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000996_285808_f2_84	2645	6417	225	74		
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000996_29314381_f2_151	2646	6418	138	45	79	0.0032

Description

pir: [LN:QQECR3] [AC:A04439] [PN:hypothetical protein E-116] [OR:Escherichia coli] [DB:pir1] [MP:72 min]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000996_29328312_c2_289	2647	6419	339	112	431	1.6e-40

Description

gp: [GI:g4927744] [LN:AF126059] [AC:AF126059] [PN:RpS19] [GN:rpsS] [OR:Streptococcus pneumoniae] [DB:genpept-bct2] [DE:Streptococcus pneumoniae isolate R6 ribosomal protein operon,partial sequence.] [NT:30S ribosomal protein S19] [LE:934] [RE:1215] [DI:direct] >gp: [GI:g4927753] [LN:AF126060] [AC:AF126060] [PN:RpS19] [GN:rpsS] [OR:Streptococcus pneumoniae] [DB:genpept-bct2] [DE:Streptococcus pneumoniae isolate ZR1 ribosomal protein operon,partial sequence.] [NT:30S ribosomal protein S19] [LE:934] [RE:1215] [DI:direct] >gp: [GI:g4927762] [LN:AF126061] [AC:AF126061] [PN:RpS19] [GN:rpsS] [OR:Streptococcus pneumoniae] [DB:genpept-bct2] [DE:Streptococcus pneumoniae isolate SP#5 ribosomal protein operon,partial sequence.] [NT:30S ribosomal protein S19] [LE:934] [RE:1215] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000996_29562550_f3_218	2648	6420	156	51		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000996_30742165_c3_347	2649	6421	1323	440	1919	3.3e-198

Description

sp: [LN:SECY\_STACA] [AC:Q05217] [GN:SECY] [OR:STAPHYLOCOCCUS CARNOSUS] [DE:PREPROTEIN TRANSLOCASE SECY SUBUNIT] [SP:Q05217] [DB:swissprot] >pir: [LN:S30115] [AC:S30115] [PN:preprotein translocase secY] [GN:secY] [CL:preprotein translocase secY] [OR:Staphylococcus carnosus] [DB:pir2] >gp: [GI:g49189] [LN:SCSECY] [AC:X70086:S47913:X68981] [GN:secY] [OR:Staphylococcus carnosus] [DB:genpept-bct1] [DE:S.carnosus secY gene.] [SP:Q05217] [LE:223] [RE:1515] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000996_3131677_f2_99	2650	6422	123	40		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000996_31377318_c1_246	2651	6423	291	96	297	2.5e-26

Description

sp: [LN:RL23\_BACSU] [AC:P42924] [GN:RPLW] [OR:BACILLUS SUBTILIS] [DE:50S RIBOSOMAL PROTEIN L23] [SP:P42924] [DB:swissprot] >pir: [LN:A69697] [AC:A69697] [PN:ribosomal protein L23] [GN:rplW] [CL:Escherichia coli ribosomal protein L23] [OR:Bacillus subtilis] [DB:pir1] >gp: [GI:d1009466:g786155] [LN:BACRPL1] [AC:D50302] [PN:Ribosomal Protein L23] [GN:rplW] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:168) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis genes for ribosomal proteins L13, L4, L23, L2, S19, L22, S3 and L16, partial and complete cds.] [LE:1140] [RE:1427] [DI:direct] >gp: [GI:e1182051:g2632385] [LN:BSUB0001] [AC:Z99104:AL009126] [PN:ribosomal protein L23] [GN:rplW] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 1 of 21): from 1 to 213080.] [SP:P42924] [LE:136990] [RE:137277] [DI:direct] >gp: [GI:g1165305] [LN:BSU43929] [AC:U43929] [PN:L23] [GN:rplW] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis ribosomal protein gene cluster, rpsJ, rplC, rplD, rplW, rplB, rpsS, rplV and rpsC genes, complete cds, and rplP gene, partial cds.] [NT:ribosomal protein] [LE:1947] [RE:2234] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000996_3304562_c3_359	2652	6424	366	121	411	2.1e-38

Description

sp: [LN:PTLA\_STAAU] [AC:P02909] [GN:LACF] [OR:STAPHYLOCOCCUS AUREUS] [EC:2.7.1.69] [DE:(EC 2.7.1.69) (EIII-LAC)] [SP:P02909] [DB:swissprot] >gp: [GI:g153037] [LN:STALACS] [AC:J03479:M17729] [OR:Staphylococcus aureus] [SR:S.aureus (strain 8325-4) DNA, clone pFB34] [DB:genpept-bct1] [DE:S.aureus enzyme III-lac (lacF), enzyme II-lac (lacE), andphospho-beta-galactosidase (lacG) genes, complete cds.] [NT:enzyme III-lac (lacF)] [LE:102] [RE:413] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000996_33437802_c2_299	2653	6425	669	222	772	1.2e-76

Description

sp: [LN:KAD\_BACSU] [AC:P16304] [GN:ADK] [OR:BACILLUS SUBTILIS] [EC:2.7.4.3] [DE:(SUPEROXIDE-INDUCIBLE PROTEIN 16) (SOI16)] [SP:P16304] [DB:swissprot] >pir: [LN:JS0492] [AC:JS0492:S12684:S08630:E69583] [PN:adenylate kinase,:ATP-AMP transphosphorylase] [GN:adk] [CL:adenylate kinase] [OR:Bacillus subtilis] [EC:2.7.4.3] [DB:pir2] >gp: [GI:g1044985] [LN:BACRPLP] [AC:L47971] [PN:adenylate kinase] [GN:adk] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis ribosomal protein (rplPNXEFROQ, rpmCDJ, rpsQNHEMK) genes, integral membrane protein (secY) gene, adenylatekinase (adk) gene, methionine aminopeptidase (map) gene,initiation factor 1 (infA) gene, RNA polymerase alpha (rpoA) gene.] [LE:6101] [RE:6754] [DI:direct] >gp: [GI:d1000951:g216340] [LN:BACSECY] [AC:D00619] [PN:adenylate kinase] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:207-21) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis genes for ribosomal proteins, SecY, adenylatekinase and methionine amino peptidase, complete cds.] [LE:2055] [RE:2708] [DI:direct] >gp: [GI:e1182070:g2632404] [LN:BSUB0001] [AC:Z99104:AL009126] [PN:adenylate kinase] [GN:adk] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:2.7.4.3] [DE:Bacillus subtilis complete genome (section 1 of 21): from 1 to 213080.] [SP:P16304] [LE:145875] [RE:146528] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000996_33463542_c2_337	2654	6426	180	59		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000996_34017517_c2_304	2655	6427	828	275	714	1.6e-70

Description

pir: [LN:F69742] [AC:F69742] [PN:hypothetical protein ybaF] [GN:ybaF] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1182080:g2632414] [LN:BSUB0001] [AC:Z99104:AL009126] [GN:ybaF] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 1 of 21): from 1 to 213080.] [LE:152128] [RE:152925] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000996_34188213_c2_295	2656	6428	423	140	579	3.3e-56

Description

gp: [GI:g1044978] [LN:BACRPLP] [AC:L47971] [PN:ribosomal protein S8] [GN:rpsH] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis ribosomal protein (rplPNXEFROQ, rpmCDJ, rpsQNHEMK) genes, integral membrane protein (secY) gene, adenylatekinase (adk) gene, methionine aminopeptidase (map) gene, initiation factor 1 (infA) gene, RNA polymerase alpha (rpoA) gene.] [LE:2198] [RE:2596] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000996_34406562_c1_259	2657	6429	867	288	644	4.2e-63

Description

pir: [LN:E69742] [AC:E69742] [PN:ABC transporter (ATP-binding protein) homolog ybaE] [GN:ybaE] [CL:ATP-binding cassette homology] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1182079:g2632413] [LN:BSUB0001] [AC:Z99104:AL009126] [GN:ybaE] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 1 of 21): from 1 to 213080.] [NT:similar to ABC transporter (ATP-binding protein)] [LE:151301] [RE:152131] [DI:direct] >gp: [GI:d1011642:g1644203] [LN:D64126] [AC:D64126] [PN:unknown] [GN:orf5] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:168) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis genes for ribosomal proteins L13 and S9, putative cell wall hydrolase CwlD, gerD protein, 16S ribosomal RNA and 23Sribosomal RNA.] [LE:861] [RE:1691] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000996_34557262_c3_384	2658	6430	135	44		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000996_34647177_c2_296	2659	6431	558	185	638	1.8e-62

Description

gp: [GI:d1039022:g4512419] [LN:AB017508] [AC:AB017508] [GN:rplF] [OR:Bacillus halodurans] [SR:Bacillus halodurans (strain:C-125) DNA] [DB:genpept-bct1] [DE:Bacillus halodurans C-125 genomic DNA, 32 kb fragment, completecds.] [NT:rplF homologue (identity of 78% to B. subtilis)] [LE:20357] [RE:20893] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000996_34651577_f2_127	2660	6432	1047	348	502	4.7e-48

Description

pir: [LN:D69756] [AC:D69756] [PN:conserved hypothetical protein yceB] [GN:yceB] [CL:ynbW protein] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:d1023111:g2415739] [LN:AB000617] [AC:AB000617] [PN:YceB] [GN:yceB] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:168 trpC2) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis genomic DNA, 22 to 25 degree region, completecds.] [NT:homologue of a hypothetical 36.6 kDa protein in] [LE:23969] [RE:24910] [DI:complement] >gp: [GI:e1182240:g2632574] [LN:BSUB0002] [AC:Z99105:AL009126] [GN:yceB] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 2 of 21): from 194651 to 415810.] [NT:similar to hypothetical proteins] [LE:115784] [RE:116725] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000996_35348182_f2_94	2661	6433	231	76		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000996_36135437_c2_287	2662	6434	648	215	676	1.7e-66

Description

sp: [LN:RL4\_BACST] [AC:P28601] [GN:RPLD] [OR:BACILLUS STEAROTHERMOPHILUS] [DE:50S RIBOSOMAL PROTEIN L4] [SP:P28601] [DB:swissprot] >pir: [LN:S24364] [AC:S24364:S36086] [PN:ribosomal protein L4] [GN:rpl4] [CL:Escherichia coli ribosomal protein L4] [OR:Bacillus stearothermophilus] [DB:pir2] >gp: [GI:g40103] [LN:BSRPLCLD] [AC:X67014:S42397] [PN:ribosomal protein L4] [GN:rplD] [OR:Bacillus stearothermophilus] [DB:genpept-bct1] [DE:B.stearothermophilus genes rplC and rplD for ribosomal proteins L3 and L4, respectively.] [SP:P28601] [LE:724] [RE:1347] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000996_36226575_c1_251	2663	6435	558	185	766	5.0e-76

Description

sp: [LN:RL5\_BACSU] [AC:P12877] [GN:RPLE] [OR:BACILLUS SUBTILIS] [DE:50S RIBOSOMAL PROTEIN L5 (BL6)] [SP:P12877] [DB:swissprot] >pir: [LN:R5BS5] [AC:S05994:A69695] [PN:ribosomal protein L5:BL6] [GN:rple] [CL:Escherichia coli ribosomal protein L5] [OR:Bacillus subtilis] [DB:pir1] >gp: [GI:g1044976] [LN:BACRPLP] [AC:L47971] [PN:ribosomal protein L5] [GN:rplE] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis ribosomal protein (rplPNXEFROQ, rpmCDJ, rpsQNHEMK) genes, integral membrane protein (secY) gene, adenylatekinase (adk) gene, methionine aminopeptidase (map) gene, initiation factor 1 (infA) gene, RNA polymerase alpha (rpoA) gene.] [LE:1419] [RE:1958] [DI:direct] >gp: [GI:g40152] [LN:BSSPC] [AC:X15664] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis S10/spc operon rpmC, rpsQ, rplN, rplX, rplE, rpsN genes.] [NT:L5 protein (AA 1-179)] [SP:P12877] [LE:1584] [RE:2123] [DI:direct] >gp: [GI:e1182061:g2632395] [LN:BSUB0001] [AC:Z99104:AL009126] [PN:ribosomal protein L5 (BL6)] [GN:rplE] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 1 of 21): from 1 to 213080.] [SP:P12877] [LE:141193] [RE:141732] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000996_4062510_f3_217	2664	6436	168	55		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000996_4100327_f3_181	2665	6437	360	119	133	6.0e-09
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Description

pir: [LN:D69798] [AC:D69798] [PN:hypothetical protein yetG] [GN:yetG] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1182694:g2633028] [LN:BSUB0004] [AC:Z99107:AL009126] [GN:yetG] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 4 of 21): from 600701 to 813890.] [LE:183921] [RE:184298] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000996_4165677_c2_305	2666	6438	807	268	544	1.7e-52
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Description

sp: [LN:TRUA\_BACSU] [AC:P70973] [GN:TRUA] [OR:BACILLUS SUBTILIS] [EC:4.2.1.70] [DE:I] (PSEUDOURIDINE SYNTHASE I) (URACIL HYDROLYASE) [SP:P70973] [DB:swissprot] >pir: [LN:F69726] [AC:F69726] [PN:pseudouridylate synthase I truA] [GN:truA] [CL:tRNA-pseudouridine synthase I] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1182081:g2632415] [LN:BSUB0001] [AC:Z99104:AL009126] [PN:pseudouridylate synthase I] [GN:truA] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:4.2.1.70] [DE:Bacillus subtilis complete genome (section 1 of 21): from 1 to 213080.] [NT:alternate gene name: ybaH] [SP:P70973] [LE:152935] [RE:153678] [DI:direct] >gp: [GI:d1011645:g1644206] [LN:D64126] [AC:D64126] [PN:unknown] [GN:orf8] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:168) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis genes for ribosomal proteins L13 and S9, putative cell wall hydrolase CwlD, gerD protein, 16S ribosomal RNA and 23Sribosomal RNA.] [LE:2496] [RE:3239] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000996_4305287_f3_211	2667	6439	123	40		
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000996_4564036_c3_363	2668	6440	1044	347	898	5.2e-90
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Description

pir: [LN:A69813] [AC:A69813] [PN:quinone oxidoreductase homolog yfmJ] [GN:yfmJ] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1182735:g2633069] [LN:BSUB0005] [AC:Z99108:AL009126] [GN:yfmJ] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 5 of 21): from 802821 to 1011250.] [NT:similar to quinone oxidoreductase] [LE:14498] [RE:15517] [DI:complement] >gp: [GI:d1023187:g2443253] [LN:D86417] [AC:D86417] [PN:YfmJ] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:AC327) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis 35.7 kb genomic DNA, 70-73 degree region,complete cds.] [LE:33004] [RE:34023] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000996_4694030_c3_367	2669	6441	1236	411	362	3.2e-33
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Description

gp: [GI:g5354197] [LN:AF157493] [AC:AF157493] [PN:putative transporter] [GN:ditE] [OR:Zymomonas mobilis] [DB:genpept] [DE:Zymomonas mobilis ZM4 fosmid clone 42D7, complete sequence.] [LE:17549] [RE:18844] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000996_4697262_c2_310	2670	6442	540	179	806	2.9e-80

Description

pir: [LN:D43258] [AC:D43258] [PN:galactose-6-phosphate isomerase subunit LacB]  
[OR:Streptococcus mutans] [DB:pir2]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000996_4714817_c2_315	2671	6443	879	292	200	1.0e-14

Description

gp: [GI:g4206189] [LN:LLU60828] [AC:U60828] [PN:unknown] [OR:Lactococcus lactis]  
[DB:genpept-bct2] [DE:Lactococcus lactis galactose-lactose operon, complete sequence.]  
[NT:orfx] [LE:12631] [RE:13554] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000996_4886592_c3_341	2672	6444	450	149	614	6.4e-60

Description

sp: [LN:RL16\_BACSU] [AC:P14577] [GN:RPLP] [OR:BACILLUS SUBTILIS] [DE:50S RIBOSOMAL PROTEIN L16] [SP:P14577] [DB:swissprot] >pir: [LN:B69696] [AC:B69696:S05989] [PN:ribosomal protein L16 (rplP)] [GN:rplP] [CL:Escherichia coli ribosomal protein L16] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1182056:g2632390] [LN:BSUB0001] [AC:Z99104:AL009126] [PN:ribosomal protein L16] [GN:rplP] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 1 of 21): from 1 to 213080.] [LE:139498] [RE:139932] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000996_4897202_c1_257	2673	6445	768	255	996	2.1e-100

Description

sp: [LN:RPOA\_BACS5] [AC:O50634] [GN:RPOA] [OR:BACILLUS SP] [SR:C-125,] [EC:2.7.7.6] [DE:ALPHA CHAIN) (RNA POLYMERASE ALPHA SUBUNIT)] [SP:O50634] [DB:swissprot] >gp: [GI:d1025104:g2760185] [LN:AB010082] [AC:AB010082] [PN:RNA polymerase alpha subunit] [GN:rpoA] [OR:Bacillus halodurans] [SR:Bacillus halodurans (strain:C-125) DNA] [DB:genpept-bct1] [DE:Bacillus halodurans C-125 gene for initiation factor IF-I, RNAPolymerase alpha subunit and ribosomal proteins, partial and complete cds.] [LE:1701] [RE:2645] [DI:direct] >gp: [GI:d1039034:g4512431] [LN:AB017508] [AC:AB017508] [GN:rpoA] [OR:Bacillus halodurans] [SR:Bacillus halodurans (strain:C-125) DNA] [DB:genpept-bct1] [DE:Bacillus halodurans C-125 genomic DNA, 32 kb fragment, completecds.] [NT:rpoA homologue (identity of 85% to B. subtilis)] [LE:26934] [RE:27878] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000996_4897253_f3_189	2674	6446	129	42		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000996_4901712_c1_261	2675	6447	408	135	496	2.0e-47

Description

pir: [LN:H69699] [AC:H69699:S11359] [PN:ribosomal protein S9 (rpsI):ribosomal protein BS10] [GN:rpsI] [CL:Escherichia coli ribosomal protein S9] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1182083:g2632417] [LN:BSUB0001] [AC:Z99104:AL009126] [PN:ribosomal protein S9] [GN:rpsI] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 1 of 21): from 1 to 213080.] [SP:P21470] [LE:154299] [RE:154691] [DI:direct] >gp: [GI:d1011647:g1644208] [LN:D64126] [AC:D64126] [PN:ribosomal protein S9] [GN:rpsI] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:168) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis genes for ribosomal proteins L13 and S9, putative cell wall hydrolase CwID, gerD protein, 16S ribosomal RNA and 23S ribosomal RNA.] [LE:3860] [RE:4252] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000996_5110637_c2_306	2676	6448	129	42		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000996_5189012_f1_55	2677	6449	168	55		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000996_55437_c2_314	2678	6450	1428	475	2439	2.6e-253

Description

sp: [LN:LACG\_STAAU] [AC:P11175] [GN:LACG] [OR:STAPHYLOCOCCUS AUREUS] [EC:3.2.1.85] [DE:GALACTOHYDROLASE] (PGALASE) (P-BETA-GAL) (PBG) [SP:P11175] [DB:swissprot] >pir: [LN:A27233] [AC:A27233] [PN:beta-galactosidase,:lactase] [CL:Agrobacterium beta-glucosidase] [OR:Staphylococcus aureus] [EC:3.2.1.23] [DB:pir2] >gp: [GI:g153039] [LN:STALACS] [AC:J03479:M17729] [OR:Staphylococcus aureus] [SR:S.aureus (strain 8325-4) DNA, clone pFB34] [DB:genpept-bct1] [DE:S.aureus enzyme III-lac (lacF), enzyme II-lac (lacE), andphospho-beta-galactosidase (lacG) genes, complete cds.] [NT:phospho-beta-galactosidase (lacG)] [LE:2149] [RE:3561] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000996_6854675_f1_20	2679	6451	279	92	119	1.8e-07

Description

pir: [LN:A69895] [AC:A69895] [PN:hypothetical protein ynzG] [GN:ynzG] [CL:hypothetical protein ynfF] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1183408:g2634133] [LN:BSUB0010] [AC:Z99113:AL009126] [GN:ynzG] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 10 of 21): from 1781201 to 2014980.] [LE:99142] [RE:99393] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000996_797308_f2_112	2680	6452	189	62		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000996_812840_c1_260	2681	6453	144	47		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000996_9771907_c2_334	2682	6454	165	54		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000997_10406642_f1_38	2683	6455	342	113	165	2.8e-12

Description

sp: [LN:NARQ\_BACSU] [AC:P39756] [GN:NARQ:NARAA] [OR:BACILLUS SUBTILIS] [DE:NARQ PROTEIN] [SP:P39756] [DB:swissprot] >pir: [LN:B69665] [AC:B69665] [PN:required for formate dehydrogenase activity narQ] [GN:narQ] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e276834:g1648855] [LN:BSATPC] [AC:Z81356] [PN:unknown] [GN:narQ] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis atpC gene.] [SP:P39756] [LE:7048] [RE:7836] [DI:direct] >gp: [GI:g580895] [LN:BSNARAAB] [AC:Z35277] [PN:unknown] [GN:narAA] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis (168) narA gene.] [SP:P39756] [LE:490] [RE:1278] [DI:direct] >gp: [GI:e1184577:g2636196] [LN:BSUB0019] [AC:Z99122:AL009126] [GN:narQ] [FN:required for formate dehydrogenase activity] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.] [NT:alternate gene name: narAA] [SP:P39756] [LE:175331] [RE:176119] [DI:complement] >gp: [GI:e1184577:g2636196] [LN:BSUB0019] [AC:Z99122:AL009126] [GN:narQ] [FN:required for formate dehydrogenase activity] [OR:Bacillus subtilis] [DB:genpept] [DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.] [NT:alternate gene name: narAA] [SP:P39756] [LE:175331] [RE:176119] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000997_1054640_f3_189	2684	6456	213	70	170	7.2e-13

Description

sp: [LN:NARQ\_BACSU] [AC:P39756] [GN:NARQ:NARAA] [OR:BACILLUS SUBTILIS] [DE:NARQ PROTEIN] [SP:P39756] [DB:swissprot] >pir: [LN:B69665] [AC:B69665] [PN:required for formate dehydrogenase activity narQ] [GN:narQ] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e276834:g1648855] [LN:BSATPC] [AC:Z81356] [PN:unknown] [GN:narQ] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis atpC gene.] [SP:P39756] [LE:7048] [RE:7836] [DI:direct] >gp: [GI:g580895] [LN:BSNARAAB] [AC:Z35277] [PN:unknown] [GN:narAA] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis (168) narA gene.] [SP:P39756] [LE:490] [RE:1278] [DI:direct] >gp: [GI:e1184577:g2636196] [LN:BSUB0019] [AC:Z99122:AL009126] [GN:narQ] [FN:required for formate dehydrogenase activity] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.] [NT:alternate gene name: narAA] [SP:P39756] [LE:175331] [RE:176119] [DI:complement] >gp: [GI:e1184577:g2636196] [LN:BSUB0019] [AC:Z99122:AL009126] [GN:narQ] [FN:required for formate dehydrogenase activity] [OR:Bacillus subtilis] [DB:genpept] [DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.] [NT:alternate gene name: narAA] [SP:P39756] [LE:175331] [RE:176119] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000997_10580182_f1_9	2685	6457	123	40		

Description

NO-HIT

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000997_10646887_f1_25	2686	6458	126	41		

Description

NO-HIT

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000997_11756250_f3_197	2687	6459	144	47		

Description

NO-HIT

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000997_11767205_f3_213	2688	6460	126	41		

Description

NO-HIT

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000997_1209800_c2_304	2689	6461	282	93	72	0.0011

Description

sp.: [LN:LACF\_AGRRD] [AC:P29823] [GN:LACF] [OR:AGROBACTERIUM RADIOBACTER] [DE:LACTOSE TRANSPORT SYSTEM PERMEASE PROTEIN LACF] [SP:P29823] [DB:swissprot] >pir:[LN:MMAGCF] [AC:S25248:S22740] [PN:membrane protein lacF] [GN:lacF] [CL:inner membrane protein ugpA] [OR:Agrobacterium radiobacter] [DB:pir1] >gp:[GI:g38969] [LN:ARLACOP] [AC:X66596:S40378:S40757] [GN:lacF] [OR:Agrobacterium radiobacter] [DB:genpept-bct1] [DE:A.radiobacter lac operon.] [SP:P29823] [LE:1897] [RE:2793] [DI:direct]

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000997_12270176_c2_349	2690	6462	180	59		

Description

NO-HIT

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503000997_12595175_f2_140	2691	6463	498	165	261	1.6e-22
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Description

sp: [LN:YKKC\_BACSU] [AC:P49856] [GN:YKKC] [OR:BACILLUS SUBTILIS] [DE:HYPOTHETICAL 11.9 KD PROTEIN IN HMP 3'REGION] [SP:P49856] [DB:swissprot] >pir:[LN:A69857] [AC:A69857] [PN:chaperonin homolog ykkC] [GN:ykkC] [CL:sugE protein] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:d1011924:g1063251] [LN:BAC168TRP2] [AC:D78189] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:168trpC2) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis hmp DNA for 7 ORFs, complete cds.] [NT:unnamed protein product] [LE:4724] [RE:5062] [DI:direct] >gp:[GI:e1181509:g2632029] [LN:BSAJ2571] [AC:AJ002571] [PN:YkkC] [GN:ykkC] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis 168 56 kb DNA fragment between xlyA and ykoR.] [SP:P49856] [LE:28642] [RE:28980] [DI:direct] >gp:[GI:e1183329:g2633663] [LN:BSUB0007] [AC:Z99110:AL009126] [GN:ykkC] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.] [NT:similar to chaperonin] [SP:P49856] [LE:181591] [RE:181929] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503000997_1375308_c2_341	2692	6464	411	136	103	9.0e-06
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Description

gp: [GI:g3283053] [LN:AF054173] [AC:AF054173] [PN:staphylococcal accessory regulator A homolog] [GN:sarA] [OR:Staphylococcus epidermidis] [DB:genpept-bct2] [DE:Staphylococcus epidermidis staphylococcal accessory regulator Ahomolog (sarA) gene, complete cds.] [LE:887] [RE:1261] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503000997_13849056_c1_251	2693	6465	279	92	79	0.041
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Description

gp: [GI:e1313955:g3392923] [LN:LLNISG] [AC:AJ000993] [PN:hypothetical protein] [GN:orfD] [OR:Lactococcus lactis] [DB:genpept-bct1] [DE:Lactococcus lactis nisG gene, orfA, orfB, orfC, and orfD.] [LE:3153] [RE:4799] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503000997_1406552_c1_252	2694	6466	123	40		
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503000997_14094002_c2_303	2695	6467	138	45		
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503000997_14097586_f3_201	2696	6468	438	145	470	1.2e-44
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Description

sp: [LN:URE2\_STAXY] [AC:P42874] [GN:UREB] [OR:STAPHYLOCOCCUS XYLOSUS] [EC:3.5.1.5] [DE:UREASE BETA SUBUNIT, (UREA AMIDOHYDROLASE)] [SP:P42874] [DB:swissprot] >pir:[LN:S38484] [AC:S38484] [PN:urease, beta chain] [CL:urease 12K chain:urease 12K chain homology] [OR:Staphylococcus xylosus] [EC:3.5.1.5] [DB:pir1] >gp:[GI:g410515] [LN:SXUREABC] [AC:X74600] [PN:urease beta subunit] [GN:ureB] [OR:Staphylococcus xylosus] [DB:genpept-bct1] [DE:S.xylosus gene for ureA, ureB, and ureC genes for urease gamma, beta and alpha subunits.] [SP:P42874] [LE:886] [RE:1299] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000997_14220635_c3_380	2697	6469	150	49		

Description

NO-HIT

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000997_14454632_c2_289	2698	6470	177	58	226	8.4e-19

Description

gp: [GI:g1022726] [LN:SHU35635] [AC:U35635] [PN:unknown] [OR:Staphylococcus haemolyticus] [SR:Staphylococcus haemolyticus strain=Y176] [DB:genpept-bct1] [DE:Staphylococcus haemolyticus IS1272 ORF1 and ORF2 genes, completecds.] [NT:ORF1] [LE:1101] [RE:1922] [DI:complement]

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000997_14460882_f1_23	2699	6471	189	62	221	2.8e-18

Description

gp: [GI:g1022726] [LN:SHU35635] [AC:U35635] [PN:unknown] [OR:Staphylococcus haemolyticus] [SR:Staphylococcus haemolyticus strain=Y176] [DB:genpept-bct1] [DE:Staphylococcus haemolyticus IS1272 ORF1 and ORF2 genes, completecds.] [NT:ORF1] [LE:1101] [RE:1922] [DI:complement]

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000997_14501888_f2_129	2700	6472	126	41		

Description

NO-HIT

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000997_14549010_c2_339	2701	6473	666	221	531	4.0e-51

Description

gp: [GI:e1429630:g4756162] [LN:A67171] [AC:A67171] [FN:MOBA GENE] [OR:Staphylococcus carnosus] [DB:genpept-pat] [DE:Sequence 11 from Patent EP0805205.] [NT:unnamed protein product] [LE:4821] [RE:5411] [DI:direct] >gp: [GI:g3955208] [LN:AF022796] [AC:AF022796] [PN:MobA] [GN:mobA] [OR:Staphylococcus carnosus] [DB:genpept-bct2] [DE:Staphylococcus carnosus molybdenum cofactor biosynthetic genecluster, complete sequence.] [NT:protein similar to MobA of Escherichia coli] [LE:7042] [RE:7632] [DI:direct]

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000997_14550133_f1_14	2702	6474	543	180		

Description

NO-HIT

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000997_15820176_f3_207	2703	6475	126	41		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000997_16129817_f1_68	2704	6476	156	51		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000997_19533567_f2_100	2705	6477	264	87	80	0.0025

Description

gp: [GI:g5306165] [LN:AF160864] [AC:AF160864] [PN:orf98] [GN:orf98] [OR:Mitochondrion Tetrahymena pyriformis] [SR:Tetrahymena pyriformis] [DB:genpept] [DE:Tetrahymena pyriformis mitochondrial DNA, complete genome.] [NT:Open reading frame ymf71 (CPGN); ATT initiation] [LE:37598] [RE:37894] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000997_20112790_c3_399	2706	6478	126	41		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000997_20345067_c3_365	2707	6479	126	41		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000997_2126925_f3_211	2708	6480	153	50		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000997_21611592_f3_236	2709	6481	369	122	89	0.0017

Description

pir: [LN:E71805] [AC:E71805] [PN:protein-export membrane protein] [GN:secF] [CL:Escherichia coli preprotein translocase chain secF] [OR:Helicobacter pylori] [SR:strain J99, , strain J99] [SR:strain J99, ] [DB:pir2] >gp: [GI:g4156068] [LN:AE001567] [AC:AE001567:AE001439] [PN:PROTEIN-EXPORT MEMBRANE PROTEIN] [GN:secF] [OR:Helicobacter pylori J99] [DB:genpept-bct2] [DE:Helicobacter pylori, strain J99 section 128 of 132 of the completest genome.] [NT:similar to H. pylori 26695 gene HP1549] [LE:9115] [RE:10086] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000997_21646015_f2_104	2710	6482	210	69	158	1.3e-11

Description

gp: [GI:g1022725] [LN:SHU35635] [AC:U35635] [PN:unknown] [OR:Staphylococcus haemolyticus] [SR:Staphylococcus haemolyticus strain=Y176] [DB:genpept-bct1] [DE:Staphylococcus haemolyticus IS1272 ORF1 and ORF2 genes, complete cds.] [NT:ORF2] [LE:394] [RE:1083] [DI:complement] >gp: [GI:g295162] [LN:STAMECRA] [AC:L14017] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus (strain COL) DNA] [DB:genpept-bct1] [DE:Staphylococcus aureus methicillin-resistance protein (mecR) gene and unknown ORF, complete cds.] [NT:unknown ORF1; putative] [LE:1492] [RE:2181] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000997_21675050_f3_230	2711	6483	360	119		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000997_21681561_f1_74	2712	6484	891	296	776	4.4e-77

Description

pir:[LN:D69744] [AC:D69744] [PN:conserved hypothetical protein ybbI] [GN:ybbI] [CL:conserved hypothetical protein b2428] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1182103:g2632437] [LN:BSUB0001] [AC:Z99104:AL009126] [GN:ybbI] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 1 of 21): from 1 to 213080.] [NT:similar to hypothetical proteins] [LE:192050] [RE:192964] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000997_21776942_c1_244	2713	6485	642	213	855	1.9e-85

Description

sp:[LN:YBXG\_BACSU] [AC:P54425:O31438] [GN:YBXG:YBDP] [OR:BACILLUS SUBTILIS] [DE:HYPOTHETICAL TRANSPORT PROTEIN IN NDHF-CSGA INTERGENIC REGION (ORF1)] [SP:P54425:O31438] [DB:swissprot] >pir:[LN:H69751] [AC:H69751:PC6045] [PN:amino acid permease homolog ybxG] [GN:ybxG] [CL:arginine permease] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:d1034070:g3599629] [LN:AB006424] [AC:AB006424] [GN:ybdP] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:168) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis genomic DNA, 70 kb region between 17 and 23degree.] [LE:29556] [RE:30944] [DI:direct] >gp:[GI:e1182158:g2632492] [LN:BSUB0002] [AC:Z99105:AL009126] [GN:ybxG] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 2 of 21): from 194651 to 415810.] [NT:alternate gene name: ybdP; similar to amino acid] [SP:P54425] [LE:31905] [RE:33293] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000997_2211433_f3_205	2714	6486	867	288	534	1.9e-51

Description

sp:[LN:URED\_BACSB] [AC:Q07400] [GN:URED] [OR:BACILLUS SP] [SR:TB-90,] [DE:UREASE ACCESSORY PROTEIN URED] [SP:Q07400] [DB:swissprot] >pir:[LN:G36950] [AC:G36950] [PN:ureD protein] [OR:Bacillus sp.] [DB:pir2] >gp:[GI:d1003839:g216366] [LN:BACUREA] [AC:D14439] [PN:urease accessory protein] [GN:UreD] [OR:Bacillus sp.] [SR:Bacillus sp. (strain:TB-90) DNA] [DB:genpept-bct1] [DE:Thermophilic Bacillus genes for urease subunits and ureaseaccessory proteins, complete cds.] [LE:4281] [RE:5096] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000997_22290657_c3_382	2715	6487	387	128	164	3.1e-12

Description

gp:[GI:g3283053] [LN:AF054173] [AC:AF054173] [PN:staphylococcal accessory regulator A homolog] [GN:sarA] [OR:Staphylococcus epidermidis] [DB:genpept-bct2] [DE:Staphylococcus epidermidis staphylococcal accessory regulator A homolog (sarA) gene, complete cds.] [LE:887] [RE:1261] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000997_22455337_f3_217	2716	6488	168	55		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000997_22692177_c1_271	2717	6489	537	178	556	9.0e-54

Description

gp: [GI:e1429621:g4756159] [LN:A67171] [AC:A67171] [FN:MOAB GENE] [OR:Staphylococcus carnosus] [DB:genpept-pat] [DE:Sequence 11 from Patent EP0805205.] [NT:unnamed protein product] [LE:1150] [RE:1662] [DI:direct] >gp: [GI:g3955202] [LN:AF022796] [AC:AF022796] [PN:MoaB] [GN:moaB] [OR:Staphylococcus carnosus] [DB:genpept-bct2] [DE:Staphylococcus carnosus molybdenum cofactor biosynthetic genecluster, complete sequence.] [NT:protein similar to MoaB of Escherichia coli] [LE:3371] [RE:3883] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000997_22734582_c2_293	2718	6490	141	46		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000997_23538332_f1_18	2719	6491	150	49		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000997_23609628_c2_330	2720	6492	975	324	385	1.2e-35

Description

gp: [GI:g2645495] [LN:AF017231] [AC:AF017231] [PN:inosine-adenosine-guanosine-nucleoside] [FN:catalyzes the hydrolysis of the N-ribosidic] [OR:Trypanosoma brucei brucei] [DB:genpept-inv1] [DE:Trypanosoma brucei brucei inosine-adenosine-guanosine-nucleosidehydrolase mRNA, complete cds.] [NT:N-ribohydrolase; IAG-nucleoside hydrolase] [LE:187] [RE:1170] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000997_23620260_c2_311	2721	6493	1107	368	334	3.0e-30

Description

sp: [LN:ODH\_ARTSP] [AC:Q44297] [GN:ODH] [OR:ARTHROBACTER SP] [SR:1C,] [EC:1.5.1.28] [DE:OPINE DEHYDROGENASE,] [SP:Q44297] [DB:swissprot] >pir: [LN:I39664] [AC:I39664] [PN:probable D-octopine dehydrogenase,] [OR:Arthrobacter sp.] [EC:1.5.1.11] [DB:pir2] >gp: [GI:d1008736:g1060848] [LN:ARGOD] [AC:D45211] [PN:opine dehydrogenase] [OR:Arthrobacter sp.] [SR:Arthrobacter sp. DNA, clone pODH1] [DB:genpept-bct1] [DE:Arthrobacter sp. gene for opine dehydrogenase, complete cds.] [LE:254] [RE:1333] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000997_23631551_c3_395	2722	6494	792	263		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000997_23642167_f3_175	2723	6495	1218	405	611	1.3e-59

Description

pir:[LN:B70065] [AC:B70065] [PN:antibiotic resistance protein homolog ywoG] [GN:ywoG] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1184551:g2636170] [LN:BSUB0019] [AC:Z99122:AL009126] [GN:ywoG] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091 to 3809700.] [NT:similar to antibiotic resistance protein] [LE:151451] [RE:152641] [DI:direct] >gp:[GI:e283116:g1684651] [LN:BSZ82987] [AC:Z82987] [PN:unknown similar to quinolone resistance protein] [GN:ywoG] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis ywo[A,B,C,D,E,F,G,H], nrg[A,B], spoIID and mb1 genes.] [LE:8662] [RE:9852] [DI:complement] >gp:[GI:e1184551:g2636170] [LN:BSUB0019] [AC:Z99122:AL009126] [GN:ywoG] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept] [DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091 to 3809700.] [NT:similar to antibiotic resistance protein] [LE:151451] [RE:152641] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000997_23678262_c3_394	2724	6496	573	190	370	4.6e-34

Description

pir:[LN:B69832] [AC:B69832] [PN:biotin biosynthesis homolog yhfU] [GN:yhfU] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1183039:g2633373] [LN:BSUB0006] [AC:Z99109:AL009126] [GN:yhfU] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 6 of 21): from 999501 to 1209940.] [NT:similar to biotin biosynthesis] [LE:111897] [RE:112457] [DI:complement] >gp:[GI:e325000:g2226257] [LN:BSY14084] [AC:Y14084] [PN:hypothetical protein] [GN:yhfU] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis chromosomal DNA, region 78-80 degrees: aprE to comK.] [NT:similarity to BioY from Bacillus sphaericus (Swiss) [LE:6325] [RE:6885] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000997_24104677_c2_291	2725	6497	1656	551	1619	2.0e-166

Description

sp:[LN:PTIB\_BACSU] [AC:P54715] [GN:GLVC:GLVCB:GLV-2] [OR:BACILLUS SUBTILIS] [EC:2.7.1.69] [DE:II, BC COMPONENT,] [SP:P54715] [DB:swissprot] >pir:[LN:G69635] [AC:G69635] [PN:PTS arbutin-like enzyme IIBC component glvC] [GN:glvC] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1182810:g2633144] [LN:BSUB0005] [AC:Z99108:AL009126] [PN:phosphotransferase system (PTS) arbutin-like] [GN:glvC] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 5 of 21): from 802821 to 1011250.] [NT:alternate gene name: yfiB] [SP:P54715] [LE:88901] [RE:90484] [DI:direct] >gp:[GI:d1009740:g1486243] [LN:D50543] [AC:D50543] [PN:unknown] [GN:glv-2] [FN:unknown] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:168, haplotype:haploid) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis DNA for 76-degree region, complete cds.] [LE:2577] [RE:4160] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000997_24257012_c1_268	2726	6498	735	244	927	4.4e-93

Description

gp:[GI:g3955199] [LN:AF022796] [AC:AF022796] [PN:ModB] [GN:modB] [OR:Staphylococcus carnosus] [DB:genpept-bct2] [DE:Staphylococcus carnosus molybdenum cofactor biosynthetic genecluster, complete sequence.] [NT:integral membrane-spanning protein of the] [LE:906] [RE:1577] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000997_24303812_c3_352	2727	6499	123	40		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000997_24314818_c2_340	2728	6500	1035	344	1410	2.9e-144

Description

gp: [GI:e1429633:g4756163] [LN:A67171] [AC:A67171] [PN:MOAA GENE] [OR:Staphylococcus carnosus] [DB:genpept-pat] [DE:Sequence 11 from Patent EP0805205.] [LE:5470] [RE:6492] [DI:direct] >gp: [GI:g3955209] [LN:AF022796] [AC:AF022796] [PN:MoaA] [GN:moaA] [OR:Staphylococcus carnosus] [DB:genpept-bct2] [DE:Staphylococcus carnosus molybdenum cofactor biosynthetic genecluster, complete sequence.] [NT:protein similar to MoaA of Escherichia coli] [LE:7691] [RE:8713] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000997_24406502_f2_127	2729	6501	171	56		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000997_24406577_c2_346	2730	6502	3156	1051	2317	2.2e-240

Description

pir: [LN:E69795] [AC:E69795] [PN:acriflavin resistance protein homolog yerP] [GN:yerP] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1182651:g2632985] [LN:BSUB0004] [AC:Z99107:AL009126] [GN:yerP] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 4 of 21): from 600701 to 813890.] [NT:similar to acriflavin resistance protein] [LE:131722] [RE:134919] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000997_24431532_c1_277	2731	6503	1254	417	1796	3.6e-185

Description

gp: [GI:g4574235] [LN:AF106850] [AC:AF106850] [PN:FmhB] [GN:fmhB] [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus FmhB (fmhB) gene, complete cds.] [NT:similar to Staphylococcus aureus FemA and FemB] [LE:204] [RE:1469] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000997_24616251_f2_148	2732	6504	696	231	139	2.6e-07

Description

gp: [GI:g567887] [LN:STMDNRN] [AC:L37338] [PN:putative repressor] [GN:dnro] [OR:Streptomyces peucetius] [SR:Streptomyces peucetius ATCC 29050 DNA] [DB:genpept-bct2] [DE:Streptomyces peucetius TDP-D-glucose-4,6-dehydratase (dnrm) gene, 3' end, regulatory protein (dnrn) gene, complete cds, and repressorprotein (dnro) gene, complete cds.] [NT:putative] [LE:1085] [RE:2107] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000997_24644008_c3_396	2733	6505	792	263	911	2.2e-91

Description

gp: [GI:g3955198] [LN:AF022796] [AC:AF022796] [PN:ModA] [GN:modA] [OR:Staphylococcus carnosus] [DB:genpept-bct2] [DE:Staphylococcus carnosus molybdenum cofactor biosynthetic genecluster, complete sequence.] [NT:molybdate-binding lipoprotein of the] [LE:109] [RE:894] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000997_24650452_f1_64	2734	6506	153	50		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000997_24804077_c3_358	2735	6507	153	50		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000997_25430317_c1_274	2736	6508	492	163	446	4.1e-42

Description

gp: [GI:g3955205] [LN:AF022796] [AC:AF022796] [PN:MobB] [GN:mobB] [OR:Staphylococcus carnosus] [DB:genpept-bct2] [DE:Staphylococcus carnosus molybdenum cofactor biosynthetic genecluster, complete sequence.] [NT:protein similar to MobB of Escherichia coli] [LE:5873] [RE:6355] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000997_25443838_c2_305	2737	6509	789	262	448	2.5e-42

Description

gp: [GI:d1023468:g2506027] [LN:D42078] [AC:D42078] [GN:NAG] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus DNA] [DB:genpept-bct1] [DE:Staphylococcus aureus DNA for N-acetyl-glucosaminidase, partialcds.] [LE:<1] [RE:1448] [DI:direct]  
>gp: [GI:d1023468:g2506027] [LN:D42078] [AC:D42078] [GN:NAG] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus DNA] [DB:genpept] [DE:Staphylococcus aureus DNA for N-acetyl-glucosaminidase, partialcds.] [LE:<1] [RE:1448] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000997_25548385_f1_7	2738	6510	144	47		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000997_25554213_f1_49	2739	6511	627	208	943	8.8e-95

Description

sp: [LN:UREG\_STAXY] [AC:P42877] [GN:UREG] [OR:STAPHYLOCOCCUS XYLOSUS] [DE:UREASE ACCESSORY PROTEIN UREG] [SP:P42877] [DB:swissprot] >gp: [GI:g511070] [LN: SXUREFG] [AC:Z35136] [PN:UreG] [OR:Staphylococcus xylosus] [DB:genpept-bct1] [DE:S.xylosus (C2a) UreF and UreG genes.] [SP:P42877] [LE:781] [RE:1395] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000997_25582885_f1_22	2740	6512	453	150	153	4.6e-11

Description

pir:[LN:C70065] [AC:C70065] [PN:transcription regulator MarR family homolog ywoH] [GN:ywoH] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1184550:g2636169] [LN:BSUB0019] [AC:Z99122:AL009126] [GN:ywoH] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.] [NT:similar to transcriptional regulator (MarR family)] [LE:151016] [RE:151429] [DI:direct] >gp:[GI:e283130:g1684652] [LN:BSZ82987] [AC:Z82987] [PN:unknown, similar to cylolysin SlyA from] [GN:ywoH] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B. subtilis ywo [A,B,C,D,E,F,G,H], nrg [A,B], spoIID and mb1 genes.] [LE:9874] [RE:10287] [DI:complement] >gp:[GI:e1184550:g2636169] [LN:BSUB0019] [AC:Z99122:AL009126] [GN:ywoH] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept] [DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.] [NT:similar to transcriptional regulator (MarR family)] [LE:151016] [RE:151429] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000997_25679762_c1_248	2741	6513	831	276	374	1.7e-34

Description

sp:[LN:SUHB\_BACSU] [AC:Q45499] [GN:SUHB] [OR:BACILLUS SUBTILIS] [DE:EXTRAGENIC SUPPRESSOR PROTEIN SUHB HOMOLOG] [SP:Q45499] [DB:swissprot] >pir:[LN:E69864] [AC:E69864] [PN:myo-inositol-1(or 4)-monophosphatase homolog yktC] [GN:yktC] [CL:suppressor protein suhB] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1185057:g2633838] [LN:BSUB0008] [AC:Z99111:AL009126] [GN:yktC] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.] [NT:similar to myo-inositol-1(or 4)-monophosphatase] [SP:Q45499] [LE:142056] [RE:142853] [DI:direct] >gp:[GI:g3282150] [LN:AF012285] [AC:AF012285:AF012284:U51911] [PN:unknown] [GN:yktC] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis mobA-nprE gene region.] [NT:similar to E. coli extragenic suppressor protein] [LE:42544] [RE:43341] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000997_26182800_c1_276	2742	6514	813	270	90	0.045

Description

sp:[LN:YCX3\_ASTLO] [AC:P34778] [OR:ASTASIA LONGA] [SR:, EUGLENOPHYCEAN ALGA] [DE:HYPOTHETICAL 20.1 KD PROTEIN IN TRNS-RPL20 INTERGENIC REGION (ORF170)] [SP:P34778] [DB:swissprot] >pir:[LN:S38600] [AC:S38600] [PN:hypothetical protein 170 (rpl20 5' region)] [OR:plastid Astasia longa] [DB:pir2] >gp:[GI:g414866] [LN:ALRIBPTR] [AC:X75653] [GN:orf170] [OR:Chloroplast Astasia longa] [SR:euglenophycean alga] [DB:genpept-pln1] [DE:A.longa plastid genes for ribosomal proteins and tRNAs.] [SP:P34778] [LE:1985] [RE:2497] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000997_26367127_f1_44	2743	6515	168	55		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000997_26375031_f1_8	2744	6516	195	64	86	0.015

Description

pir: [LN:A70387] [AC:A70387] [PN:conserved hypothetical protein aq\_1006] [GN:aq\_1006] [OR: *Aquifex aeolicus*] [DB:pir2] >gp: [GI:g2983515] [LN:AE000718] [AC:AE000718:AE000657] [PN:hypothetical protein] [GN:aq\_1006] [OR: *Aquifex aeolicus*] [DB:genpept-bct2] [DE: *Aquifex aeolicus* section 50 of 109 of the complete genome.] [LE:2797] [RE:5733] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000997_26758426_c2_316	2745	6517	750	249	121	2.8e-07
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Description

gp: [GI:g3283053] [LN:AF054173] [AC:AF054173] [PN:staphylococcal accessory regulator A homolog] [GN:sarA] [OR: *Staphylococcus epidermidis*] [DB:genpept-bct2] [DE: *Staphylococcus epidermidis* staphylococcal accessory regulator Ahomolog (sarA) gene, complete cds.] [LE:887] [RE:1261] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000997_29494067_c3_356	2746	6518	213	70	50	0.031
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Description

pir: [LN:PC1133] [AC:PC1133:S18087] [PN:hypothetical protein 119 (rmpG 5' region)] [OR: *Lactococcus lactis*] [DB:pir2]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000997_29697752_c2_302	2747	6519	786	261	499	9.8e-48
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Description

sp: [LN:LYTR\_BACSU] [AC:Q02115] [GN:LYTR] [OR: *BACILLUS SUBTILIS*] [DE:MEMBRANE-BOUND PROTEIN LYTR] [SP:Q02115] [DB:swissprot] >pir: [LN:A47679] [AC:A47679:H69654] [PN:lyt divergon expression attenuator LytR] [GN:lytR] [CL: *Bacillus subtilis* probable transcription regulator yvhJ] [OR: *Bacillus subtilis*] [DB:pir2] >gp: [GI:g143156] [LN:BACLYTABCD] [AC:M87645] [PN:membrane bound protein] [GN:lytR] [OR: *Bacillus subtilis*] [SR: *Bacillus subtilis* (strain W168) DNA] [DB:genpept-bct1] [DE: *Bacillus subtilis* membrane bound protein (lytA and lytR); amidase enhancer (lytB); and amidase (lytC) genes, complete cds's.] [LE:92] [RE:1012] [DI:complement] >gp: [GI:e1184471:g2636091] [LN:BSUB0019] [AC:Z99122:AL009126] [PN:membrane-bound protein] [GN:lytR] [FN:attenuator role for lytABC and lytR expression] [OR: *Bacillus subtilis*] [DB:genpept-bct1] [DE: *Bacillus subtilis* complete genome (section 19 of 21): from 3597091 to 3809700.] [SP:Q02115] [LE:65251] [RE:66171] [DI:direct] >gp: [GI:e1184471:g2636091] [LN:BSUB0019] [AC:Z99122:AL009126] [PN:membrane-bound protein] [GN:lytR] [FN:attenuator role for lytABC and lytR expression] [OR: *Bacillus subtilis*] [DB:genpept] [DE: *Bacillus subtilis* complete genome (section 19 of 21): from 3597091 to 3809700.] [SP:Q02115] [LE:65251] [RE:66171] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000997_31284550_f3_237	2748	6520	174	57		
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000997_3250075_f3_220	2749	6521	1008	335	705	1.5e-69

Description

pir: [LN:A71175] [AC:A71175] [PN:probable dehydrogenase] [GN:PH0597] [OR:Pyrococcus horikoshii] [DB:pir2] >gp: [GI:d1030629:g3257003] [LN:AP000002] [AC:AP000002:AB009475:AB009476:AB009477:AB009478:AB009479:AB009480] [PN:376aa long hypothetical dehydrogenase] [GN:PH0597] [OR:Pyrococcus horikoshii] [SR:Pyrococcus horikoshii (strain:OT3) DNA] [DB:genpept-bct1] [DE:Pyrococcus horikoshii OT3 genomic DNA, 287001-544000 nt. position(2/7).] [NT:similar to owl:BSZ9404317 percent identity: 49.821] [LE:248539] [RE:249669] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000997_33360910_f3_216	2750	6522	549	182	120	1.4e-07

Description

pir: [LN:S74932] [AC:S74932] [PN:hypothetical protein slr0686] [OR:Synechocystis sp.] [SR:PCC 6803, , PCC 6803] [SR:PCC 6803, ] [DB:pir2] >gp: [GI:d1017705:g1652047] [LN:D90902] [AC:D90902:AB001339] [PN:hypothetical protein] [OR:Synechocystis sp.] [SR:Synechocystis sp. (strain:PCC6803) DNA] [DB:genpept-bct1] [DE:Synechocystis sp. PCC6803 complete genome, 4/27, 402290-524345.] [NT:ORF\_ID:slr0686] [LE:27521] [RE:27880] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000997_33694505_f3_198	2751	6523	162	53	47	0.0063

Description

gp: [GI:d1042768:g5103471] [LN:AP000058] [AC:AP000058] [PN:102aa long hypothetical protein] [GN:APE0083] [OR:Aeropyrum pernix] [SR:Aeropyrum pernix (strain:K1) DNA] [DB:genpept] [DE:Aeropyrum pernix genomic DNA, section 1/7.] [LE:56764] [RE:57072] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000997_3371062_f1_10	2752	6524	333	110	90	0.00034

Description

gp: [GI:g1040951] [LN:AOU35271] [AC:U35271] [PN:NADH dehydrogenase subunit 6] [OR:Mitochondrion Anopheles oswaldoi] [SR:Anopheles oswaldoi] [DB:genpept-inv1] [DE:Anopheles oswaldoi NADH dehydrogenase subunit 6 gene, mitochondrial gene encoding mitochondrial product, partial cds.] [LE:<1] [RE:525] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000997_34192165_f1_63	2753	6525	345	114	264	7.9e-23

Description

pir: [LN:B69857] [AC:B69857] [PN:chaperonin homolog ykkD] [GN:ykkD] [CL:sugE protein] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1181510:g2632030] [LN:BSAJ2571] [AC:AJ002571] [PN:YkkD] [GN:ykkD] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis 168 56 kb DNA fragment between xlyA and ykoR.] [LE:28980] [RE:29297] [DI:direct] >gp: [GI:e1183330:g2633664] [LN:BSUB0007] [AC:Z99110:AL009126] [GN:ykkD] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 7 of 21): from 1194391 to 1411140.] [NT:similar to chaperonin] [LE:181929] [RE:182246] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503000997_34411552_f2_123	2754	6526	1722	573	2703	2.8e-281
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Description

sp: [LN:URE1\_STAXY] [AC:P42873] [GN:UREC] [OR:STAPHYLOCOCCUS XYLOSUS] [EC:3.5.1.5] [DE:UREASE ALPHA SUBUNIT, (UREA AMIDOHYDROLASE)] [SP:P42873] [DB:swissprot] >pir: [LN:S38485] [AC:S38485] [PN:urease, 62K chain:urease alpha chain] [GN:ureC] [CL:urease 62K chain:urease 62K chain homology] [OR:Staphylococcus xylosus] [EC:3.5.1.5] [DB:pir2] >gp: [GI:g410516] [LN: SXUREABC] [AC:X74600] [PN:urease alpha subunit] [GN:ureC] [OR:Staphylococcus xylosus] [DB:genpept-bct1] [DE:S.xylosus gene for ureA, ureB, and ureC genes for urease gamma,beta and alpha subunits.] [SP:P42873] [LE:1296] [RE:3011] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503000997_34430_f2_96	2755	6527	156	51		
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503000997_34431300_c2_300	2756	6528	774	257	139	2.8e-09
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Description

gp: [GI:d1011987:g1402529] [LN:D78257] [AC:D78257] [PN:ORF8] [GN:orf8] [OR:Enterococcus faecalis] [SR:Enterococcus faecalis plasmid:pYI17 DNA] [DB:genpept-bct1] [DE:Enterococcus faecalis plasmid pYI17 genes for BacA, BacB, ORF3,ORF4, ORF5, ORF6, ORF7, ORF8, ORF9, ORF10, ORF11,partial cds.] [LE:1899] [RE:2261] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503000997_34617187_f2_156	2757	6529	207	68	74	0.00010
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Description

gp: [GI:g4164553] [LN:AF081828] [AC:AF081828] [PN:NADH dehydrogenase 6] [OR:Mitochondrion Ixodes hexagonus] [SR:Ixodes hexagonus] [DB:genpept-inv2] [DE:Ixodes hexagonus mitochondrial DNA, complete genome.] [LE:9406] [RE:9831] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503000997_35191527_f1_19	2758	6530	156	51		
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503000997_35319025_f3_200	2759	6531	132	43		
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000997_35547892_f3_218	2760	6532	156	51	161	8.5e-12

Description

gp: [GI:g2735506] [LN:SCU96107] [AC:U96107] [PN:SceB precursor] [GN:sceB] [OR:Staphylococcus carnosus] [DB:genpept-bct2] [DE:Staphylococcus carnosus N5,N10-methylenetetrahydromethanopterinreductase homolog, SceB precursor (sceB) and putative transmembraneprotein genes, complete cds, and putative Na+/H+ antiporter NhaC(nhaC) gene, partial cds.] [NT:major secreted protein] [LE:1894] [RE:2685] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000997_35572051_f1_72	2761	6533	129	42		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000997_36017151_f2_110	2762	6534	141	46		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000997_36113805_c1_245	2763	6535	750	249	775	5.6e-77

Description

sp: [LN:YBXG\_BACSU] [AC:P54425:031438] [GN:YBXG:YBDP] [OR:BACILLUS SUBTILIS] [DE:HYPOTHETICAL TRANSPORT PROTEIN IN NDHF-CSGA INTERGENIC REGION (ORF1)] [SP:P54425:031438] [DB:swissprot] >pir: [LN:H69751] [AC:H69751:PC6045] [PN:amino acid permease homolog ybxG] [GN:ybxG] [CL:arginine permease] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:d1034070:g3599629] [LN:AB006424] [AC:AB006424] [GN:ybdP] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:168) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis genomic DNA, 70 kb region between 17 and 23degree.] [LE:29556] [RE:30944] [DI:direct] >gp: [GI:e1182158:g2632492] [LN:BSUB0002] [AC:Z99105:AL009126] [GN:ybxG] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 2 of 21): from 194651 to 415810.] [NT:alternate gene name: ybdP; similar to amino acid] [SP:P54425] [LE:31905] [RE:33293] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000997_36132792_c3_402	2764	6536	255	84	218	5.9e-18

Description

gp: [GI:e1429627:g4756161] [LN:A67171] [AC:A67171] [PN:MOAD GENE] [OR:Staphylococcus carnosus] [DB:genpept-pat] [DE:Sequence 11 from Patent EP0805205.] [LE:4583] [RE:4816] [DI:direct] >gp: [GI:g3955207] [LN:AF022796] [AC:AF022796] [PN:MoaD] [GN:moaD] [OR:Staphylococcus carnosus] [DB:genpept-bct2] [DE:Staphylococcus carnosus molybdenum cofactor biosynthetic genecluster, complete sequence.] [NT:protein similar to MoaD of Escherichia coli] [LE:6804] [RE:7037] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000997_36134427_c1_241	2765	6537	657	218	251	1.9e-21

Description

sp: [LN:YHCW\_BACSU] [AC:P54607] [GN:YHCW] [OR:BACILLUS SUBTILIS] [DE:HYPOTHETICAL 24.7 KD PROTEIN IN CSPB-GLPP INTERGENIC REGION] [SP:P54607] [DB:swissprot] >pir:[LN:C69824] [AC:C69824] [PN:phosphoglycolate phosphatase homolog yhcW] [GN:yhcW] [CL:hypothetical protein b2690] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e233881:g1239999] [LN:BS75DGREG] [AC:X96983] [PN:hypothetical protein] [GN:yhcW] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B. subtilis chromosomal DNA (region 75 degrees: cspB upstream of glpPFKD operon).] [NT:similarity to phosphoglycolate phosphatase from] [SP:P54607] [LE:18604] [RE:19266] [DI:direct] >gp:[GI:e1182913:g2633247] [LN:BSUB0005] [AC:Z99108:AL009126] [GN:yhcW] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 5 of 21): from 802821 to 1011250.] [NT:similar to phosphoglycolate phosphatase] [SP:P54607] [LE:194410] [RE:195072] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000997_36209660_f2_116	2766	6538	378	125		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000997_36225625_f1_56	2767	6539	795	264	1034	2.0e-104

Description

gp: [GI:e244971:g1340128] [LN:SA1234] [AC:X97985] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:S. aureus orfs 1,2,3 & 4.] [NT:ORF1] [LE:537] [RE:1304] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000997_36615903_c2_329	2768	6540	1164	387	1007	1.5e-101

Description

pir: [LN:H69771] [AC:H69771] [PN:butyryl-CoA dehydrogenase homolog ydbM] [GN:ydbM] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:d1020042:g1881262] [LN:AB001488] [AC:AB001488] [GN:ydbM] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:168) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis genome sequence, 148 kb sequence of the region between 35 and 47 degree.] [NT:SIMILAR TO ACYL-COA DEHYDROGENASE.] [LE:38215] [RE:39360] [DI:direct] >gp:[GI:e1182418:g2632752] [LN:BSUB0003] [AC:Z99106:AL009126] [GN:ydbM] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 3 of 21): from 402751 to 611850.] [NT:similar to butyryl-CoA dehydrogenase] [LE:101959] [RE:103104] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000997_3943752_f2_128	2769	6541	150	49		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000997_3947153_f3_204	2770	6542	456	151	482	6.2e-46

Description

sp: [LN:UREE\_BACSB] [AC:Q07401] [GN:UREE] [OR:BACILLUS SP] [SR:TB-90,] [DE:UREASE ACCESSORY PROTEIN UREE] [SP:Q07401] [DB:swissprot] >pir:[LN:D36950] [AC:D36950] [PN:ureE protein] [OR:Bacillus sp.] [DB:pir2] >gp:[GI:d1003836:g393297] [LN:BACUREA] [AC:D14439] [PN:urease accessory protein] [GN:UreE] [OR:Bacillus sp.] [SR:Bacillus sp. (strain:TB-90) DNA] [DB:genpept-bct1] [DE:Thermophilic Bacillus genes for urease subunits and ureaseaccessory proteins, complete cds.] [LE:2521] [RE:2967] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000997_3991557_f1_55	2771	6543	141	46		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000997_4042327_c3_390	2772	6544	918	305	309	1.3e-27

Description

gp: [GI:g1322222] [LN:HSU35735] [AC:U35735] [PN:RACH1] [GN:RACH1] [OR:Homo sapiens] [SR:human] [DB:genpept-pri2] [DE:Human RACH1 (RACH1) mRNA, complete cds.] [LE:169] [RE:1338] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000997_4086568_c3_381	2773	6545	1983	660	130	1.8e-07

Description

sp: [LN:SOXS\_ECOLI] [AC:P22539] [GN:SOXS] [OR:ESCHERICHIA COLI] [DE:REGULATORY PROTEIN SOXS] [SP:P22539] [DB:swissprot]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000997_42500_f1_24	2774	6546	159	52		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000997_4459380_f1_84	2775	6547	207	68		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000997_4459505_c2_343	2776	6548	129	42		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000997_4486693_f2_92	2777	6549	804	267	976	2.8e-98

Description

gp: [GI:e324856:g2226002] [LN:SXY14043] [AC:Y14043] [PN:glucose-1-dehydrogenase] [GN:gdh] [OR:Staphylococcus xylosus] [DB:genpept-bct1] [DE:Staphylococcus xylosus glcU and gdh genes.] [LE:1222] [RE:2013] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000997_4491450_f2_150	2778	6550	873	290	310	1.0e-27

Description

gp: [GI:g4980827] [LN:AE001714] [AC:AE001714:AE000512] [PN:transcriptional regulator, RpiR family] [GN:TM0326] [OR:Thermotoga maritima] [DB:genpept-bct2] [DE:Thermotoga maritima section 26 of 136 of the complete genome.] [NT:similar to SP:P46118 PID:881368 GB:U00096] [LE:3706] [RE:4548] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000997_4547163_f1_48	2779	6551	699	232	741	2.2e-73

Description

sp: [LN:UREF\_STAXY] [AC:P42876] [GN:UREF] [OR:STAPHYLOCOCCUS XYLOSUS] [DE:UREASE ACCESSORY PROTEIN UREF] [SP:P42876] [DB:swissprot] >gp: [GI:g511069] [LN: SXUREFG] [AC:Z35136] [PN:Uref] [OR:Staphylococcus xylosus] [DB:genpept-bct1] [DE:S.xylosus (C2a) Uref and UreG genes.] [SP:P42876] [LE:79] [RE:648] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000997_4569012_f1_79	2780	6552	588	195		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000997_4720290_f2_145	2781	6553	138	45		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000997_4720928_f1_11	2782	6554	186	61		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000997_4726550_f2_143	2783	6555	177	58		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000997_4800202_c1_269	2784	6556	621	206	694	2.1e-68

Description

gp: [GI:g3955200] [LN:AF022796] [AC:AF022796] [PN:ModC] [GN:modC] [OR:Staphylococcus carnosus] [DB:genpept-bct2] [DE:Staphylococcus carnosus molybdenum cofactor biosynthetic genecluster, complete sequence.] [NT:ATP-binding protein of the molybdate-specific ABC] [LE:1578] [RE:2186] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000997_4804153_f1_33	2785	6557	690	229	618	2.4e-60

Description

gp: [GI:e1429636:g4756164] [LN:A67171] [AC:A67171] [FN:MOAC GENE] [OR:Staphylococcus carnosus] [DB:genpept-pat] [DE:Sequence 11 from Patent EP0805205.] [NT:unnamed protein product] [LE:1846] [RE:2331] [DI:complement] >gp: [GI:g3955203] [LN:AF022796] [AC:AF022796] [PN:MoaC] [GN:moaC] [OR:Staphylococcus carnosus] [DB:genpept-bct2] [DE:Staphylococcus carnosus molybdenum cofactor biosynthetic genecluster, complete sequence.] [NT:protein similar to MoaC of Escherichia coli] [LE:4067] [RE:4552] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000997_4876675_f2_122	2786	6558	399	132	430	2.0e-40

Description

sp: [LN:URE3\_STAXY] [AC:P42875] [GN:UREA] [OR:STAPHYLOCOCCUS XYLOSUS] [EC:3.5.1.5] [DE:UREASE GAMMA SUBUNIT, (UREA AMIDOHYDROLASE)] [SP:P42875] [DB:swissprot] >pir: [LN:S38483] [AC:S38483] [PN:urease, 11K chain:urease gamma chain] [CL:urease 11K chain:urease 11K chain homology] [OR:Staphylococcus xylosus] [EC:3.5.1.5] [DB:pir2] >gp: [GI:g581787] [LN:SXUREABC] [AC:X74600] [PN:urease gamma subunit] [GN:ureA] [OR:Staphylococcus xylosus] [DB:genpept-bct1] [DE:S.xylosus gene for ureA, ureB, and ureC genes for urease gamma,beta and alpha subunits.] [SP:P42875] [LE:568] [RE:870] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000997_4884662_c3_367	2787	6559	1128	375	333	1.0e-32

Description

gp: [GI:e1393931:g4490992] [LN:SCE29] [AC:AL035707] [PN:putative salicylate hydroxylase] [GN:SCE29.14c] [OR:Streptomyces coelicolor] [DB:genpept-bct1] [DE:Streptomyces coelicolor cosmid E29.] [NT:SCE29.14c, possible salicylate hydroxylase, len:] [LE:19076] [RE:20338] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000997_4976687_c1_281	2788	6560	924	307	232	1.9e-19

Description

gp: [GI:g4980727] [LN:AE001707] [AC:AE001707:AE000512] [PN:conserved hypothetical protein] [GN:TM0229] [OR:Thermotoga maritima] [DB:genpept-bct2] [DE:Thermotoga maritima section 19 of 136 of the complete genome.] [NT:similar to GB:L77117 PID:1591686 percent identity:] [LE:5630] [RE:6487] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000997_5082812_c2_310	2789	6561	135	44		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000997_5087556_c2_335	2790	6562	849	282	990	9.2e-100

Description

gp: [GI:e1429618:g4756158] [LN:A67171] [AC:A67171] [FN:MOEB GENE] [OR:Staphylococcus carnosus] [DB:genpept-pat] [DE:Sequence 11 from Patent EP0805205.] [NT:unnamed protein product] [LE:117] [RE:1118] [DI:direct] >gp: [GI:g3955201] [LN:AF022796] [AC:AF022796] [PN:MoeB] [GN:moeB] [OR:Staphylococcus carnosus] [DB:genpept-bct2] [DE:Staphylococcus carnosus molybdenum cofactor biosynthetic genecluster, complete sequence.] [NT:protein similar to the molybdopterin synthase] [LE:2338] [RE:3339] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000997_5113550_f2_149	2791	6563	1089	362	269	2.3e-23

Description

pir: [LN:C70217] [AC:C70217] [PN:outer surface protein homolog] [OR: *Borrelia burgdorferi*] [SR:, Lyme disease spirochete] [DB:pir2] >gp: [GI:g2689897] [LN:AE000792] [AC:AE000792] [PN:outer surface protein, putative] [GN:BBB07] [OR: *Borrelia burgdorferi*] [SR:Lyme disease spirochete] [DB:genpept-bct2] [DE: *Borrelia burgdorferi* plasmid cp26, complete plasmid sequence.] [NT:similar to GB:M88764 SP:Q09090 PID:469166] [LE:4769] [RE:5866] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000997_5266018_f2_160	2792	6564	771	256	415	7.8e-39

Description

sp: [LN:YFIA\_BACSU] [AC:P54717] [GN:YFIA] [OR: *BACILLUS SUBTILIS*] [DE:HYPOTHETICAL 29.3 KD PROTEIN IN GLVG-GLVBC INTERGENIC REGION] [SP:P54717] [DB:swissprot] >pir: [LN:D69802] [AC:D69802] [PN:conserved hypothetical protein yfia] [GN:yfia] [OR: *Bacillus subtilis*] [DB:pir2] >gp: [GI:e1182809:g2633143] [LN:BSUB0005] [AC:Z99108:AL009126] [GN:yfia] [FN:unknown] [OR: *Bacillus subtilis*] [DB:genpept-bct1] [DE: *Bacillus subtilis* complete genome (section 5 of 21): from 802821 to 1011250.] [NT:similar to hypothetical proteins] [SP:P54717] [LE:88122] [RE:88886] [DI:direct] >gp: [GI:d1009739:g1486242] [LN:D50543] [AC:D50543] [PN:unknown] [GN:yfia] [FN:unknown] [OR: *Bacillus subtilis*] [SR: *Bacillus subtilis* (strain:168, haplotype:haploid) DNA] [DB:genpept-bct1] [DE: *Bacillus subtilis* DNA for 76-degree region, complete cds.] [LE:1798] [RE:2562] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000997_5898328_f2_91	2793	6565	864	287	1102	1.2e-111

Description

gp: [GI:e324855:g2226001] [LN:SXY14043] [AC:Y14043] [PN:glucose uptake protein] [GN:glcU] [OR: *Staphylococcus xylosus*] [DB:genpept-bct1] [DE: *Staphylococcus xylosus* glcU and gdh genes.] [LE:306] [RE:1172] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000997_6050010_c3_404	2794	6566	129	42		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000997_6757755_f2_121	2795	6567	171	56		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000997_6929676_c1_255	2796	6568	342	113		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000997_7031318_f2_153	2797	6569	339	112		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000997_7086677_c3_364	2798	6570	243	80	78	0.019

Description

sp: [LN:LY4F\_MOUSE] [AC:Q60653] [GN:LY49F:LY-49F:LY49-F] [OR:MUS MUSCULUS] [SR:, MOUSE] [DE:T-CELL SURFACE GLYCOPROTEIN LY-49F (LY49-F ANTIGEN)] [SP:Q60653] [DB:swissprot] >pir: [LN:I49051] [AC:I49051] [PN:Ly-49F-GE antigen] [OR:Mus musculus] [SR:, house mouse] [DB:pir2] >gp: [GI:g533492] [LN:MMU10092] [AC:U10092] [PN:Ly-49F-GE antigen] [OR:Mus musculus] [SR:house mouse] [DB:genpept-rod] [DE:Mus musculus C57BL/6 Ly-49F-GE antigen mRNA, complete cds.] [LE:81] [RE:881] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000997_818812_c2_337	2799	6571	1287	428	1560	3.6e-160

Description

gp: [GI:e1429624:g4756160] [LN:A67171] [AC:A67171] [FN:MOEA GENE] [OR:Staphylococcus carnosus] [DB:genpept-pat] [DE:Sequence 11 from Patent EP0805205.] [NT:unnamed protein product] [LE:2396] [RE:3655] [DI:direct] >gp: [GI:g3955204] [LN:AF022796] [AC:AF022796] [PN:MoeA] [GN:moeA] [OR:Staphylococcus carnosus] [DB:genpept-bct2] [DE:Staphylococcus carnosus molybdenum cofactor biosynthetic genecluster, complete sequence.] [NT:protein similar to MoeA of Escherichia coli] [LE:4617] [RE:5876] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000997_829761_c1_288	2800	6572	2172	723	1751	2.1e-180

Description

pir: [LN:H69724] [AC:H69724] [PN:DNA topoisomerase III topB] [GN:topB] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:d1020016:g1881236] [LN:AB001488] [AC:AB001488] [PN:PROBABLE DNA TOPOISOMERASE III] [GN:topB] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:168) DNA] [DB:genpept-bct1] [EC:5.99.1.2] [DE:Bacillus subtilis genome sequence, 148 kb sequence of the region between 35 and 47 degree.] [LE:9617] [RE:11800] [DI:direct] >gp: [GI:e1182392:g2632726] [LN:BSUB0003] [AC:Z99106:AL009126] [PN:DNA topoisomerase III] [GN:topB] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:5.99.1.2] [DE:Bacillus subtilis complete genome (section 3 of 21): from 402751 to 611850.] [LE:73361] [RE:75544] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000997_834686_c2_290	2801	6573	132	43		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000997_959427_f1_62	2802	6574	417	138	241	2.2e-20

Description

gp: [GI:g2735506] [LN:SCU96107] [AC:U96107] [PN:SceB precursor] [GN:sceB] [OR:Staphylococcus carnosus] [DB:genpept-bct2] [DE:Staphylococcus carnosus N5,N10-methylenetetrahydromethanopterinreductase homolog, SceB precursor (sceB) and putative transmembraneprotein genes, complete cds, and putative Na+/H+ antiporter NhaC(nhaC) gene, partial cds.] [NT:major secreted protein] [LE:1894] [RE:2685] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000997_964077_c1_275	2803	6575	453	150	659	1.1e-64

Description

gp: [GI:g3955206] [LN:AF022796] [AC:AF022796] [PN:MoaE] [GN:moaE] [OR:Staphylococcus carnosus] [DB:genpept-bct2] [DE:Staphylococcus carnosus molybdenum cofactor biosynthetic genecluster, complete sequence.] [NT:protein similar to MoaE of Escherichia coli] [LE:6352] [RE:6804] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000997_975061_c3_377	2804	6576	1455	484	916	6.4e-92

Description

sp: [LN:YB07\_HAEIN] [AC:Q57007:P96339] [GN:HI1107] [OR:HAEMOPHILUS INFLUENZAE] [DE:HYPOTHETICAL NA+/H+ ANTIPORTER HI1107] [SP:Q57007:P96339] [DB:swissprot] >pir: [LN:I64182] [AC:I64182] [PN:Na+/H+-exchanging protein homolog:Na+/H+ antiporter] [CL:Na+/H+-exchanging protein] [OR:Haemophilus influenzae] [DB:pir2] >gp: [GI:g1574661] [LN:U32790] [AC:U32790:L42023] [PN:Na+/H+ antiporter (nhaC)] [GN:HI1107] [OR:Haemophilus influenzae Rd] [DB:genpept-bct2] [DE:Haemophilus influenzae Rd section 105 of 163 of the completegenome.] [NT:similar to GB:M73530 SP:P27611 PID:143245] [LE:7526] [RE:8932] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000997_9845631_f3_222	2805	6577	156	51		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000997_9928188_f1_39	2806	6578	132	43	95	0.00025

Description

sp: [LN:NARQ\_BACSU] [AC:P39756] [GN:NARQ:NARAA] [OR:BACILLUS SUBTILIS] [DE:NARQ PROTEIN] [SP:P39756] [DB:swissprot] >pir: [LN:B69665] [AC:B69665] [PN:required for formate dehydrogenase activity narQ] [GN:narQ] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e276834:g1648855] [LN:BSATPC] [AC:Z81356] [PN:unknown] [GN:narQ] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis atpC gene.] [SP:P39756] [LE:7048] [RE:7836] [DI:direct] >gp: [GI:g580895] [LN:BSNARAAB] [AC:Z35277] [PN:unknown] [GN:narAA] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis (168) narA gene.] [SP:P39756] [LE:490] [RE:1278] [DI:direct] >gp: [GI:e1184577:g2636196] [LN:BSUB0019] [AC:Z99122:AL009126] [GN:narQ] [FN:required for formate dehydrogenase activity] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091 to 3809700.] [NT:alternate gene name: narAA] [SP:P39756] [LE:175331] [RE:176119] [DI:complement] >gp: [GI:e1184577:g2636196] [LN:BSUB0019] [AC:Z99122:AL009126] [GN:narQ] [FN:required for formate dehydrogenase activity] [OR:Bacillus subtilis] [DB:genpept] [DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091 to 3809700.] [NT:alternate gene name: narAA] [SP:P39756] [LE:175331] [RE:176119] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000997_9928500_c1_270	2807	6579	261	86	286	3.7e-25

Description

gp: [GI:e1429618:g4756158] [LN:A67171] [AC:A67171] [FN:MOEB GENE] [OR:Staphylococcus carnosus] [DB:genpept-pat] [DE:Sequence 11 from Patent EP0805205.] [NT:unnamed protein product] [LE:117] [RE:1118] [DI:direct] >gp: [GI:g3955201] [LN:AF022796] [AC:AF022796] [PN:MoeB] [GN:moeB] [OR:Staphylococcus carnosus] [DB:genpept-bct2] [DE:Staphylococcus carnosus molybdenum cofactor biosynthetic genecluster, complete sequence.] [NT:protein similar to the molybdopterin synthase] [LE:2338] [RE:3339] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000997_9977318_f1_75	2808	6580	1437	478	700	4.9e-69

Description

pir: [LN:D65017] [AC:D65017] [PN:hypothetical protein b2429] [CL:phosphotransferase system sucrose-specific enzyme II, factor II] [OR:Escherichia coli] [DB:pir2] >gp: [GI:d1017042:g1799859] [LN:D90872] [AC:D90872:AB001340] [PN:PTS SYSTEM, SUCROSE-SPECIFIC IIBC COMPONENT] [GN:IPA-49D] [OR:Escherichia coli] [SR:Escherichia coli (strain:K12) DNA, clone\_lib:Kohara lambda minise] [DB:genpept-bct1] [DE:E.coli genomic DNA, Kohara clone #419(54.7-55.1 min.)] [NT:similar to [SwissProt Accession Number P05306]] [LE:9801] [RE:11225] [DI:direct] >gp: [GI:d1017045:g1799863] [LN:D90873] [AC:D90873:AB001340] [PN:PTS SYSTEM, SUCROSE-SPECIFIC IIBC COMPONENT] [GN:IPA-49D] [OR:Escherichia coli] [SR:Escherichia coli (strain:K12) DNA, clone\_lib:Kohara lambda minise] [DB:genpept-bct1] [DE:E.coli genomic DNA, Kohara clone #420(54.9-55.2 min.)] [NT:similar to [SwissProt Accession Number P05306]] [LE:611] [RE:2035] [DI:direct] >gp: [GI:g1788769] [LN:AE000330] [AC:AE000330:U00096] [PN:putative PTS enzyme II] [GN:b2429] [FN:putative enzyme; Not classified] [OR:Escherichia coli] [DB:genpept-bct2] [DE:Escherichia coli K-12 MG1655 section 220 of 400 of the complete genome.] [NT:o474; 33 pct identical (29 gaps) to 436 residues] [LE:5237] [RE:6661] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000998_10159760_f1_50	2809	6581	156	51		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000998_10312805_f3_197	2810	6582	144	47		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000998_10646950_c1_238	2811	6583	1221	406	1151	8.0e-117

Description

pir: [LN:A69974] [AC:A69974] [PN:cystathione gamma-synthase homolog yrhB] [GN:yrhB] [CL:O-succinylhomoserine (thiol)-lyase] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:g1934606] [LN:BSU93874] [AC:U93874] [PN:cystathione gamma-lyase] [GN:yrhB] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis cysteine synthase (yrhA), cystathioninegamma-lyase (yrhB), YrhC (yrhC), YrhD (yrhD), formate dehydrogenasechain A (yrhE), YrhF (yrhF), formate dehydrogenase (yrhG), YrhH(yrhH), regulatory protein (yrhI), cytochrome P450 102 (yrhJ), YrhK(yrhK), hypothetical protein YrhL (yrhL), putative anti-SigV factor(yrhM), RNA polymerase sigma factor SigV (sigV) and YrhO (yrhO)genes, complete cds, and YrhP (yrhP) gene, partial cds.] [NT:similar to Rattus norvegicus cystathione] [LE:986] [RE:2125] [DI:direct] >gp: [GI:e1183955:g2635171] [LN:BSUB0014] [AC:Z99117:AL009126] [GN:yrhB] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.] [NT:similar to cystathione gamma-synthase] [LE:184821] [RE:185960] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000998_10723177_f1_59	2812	6584	255	84		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000998_11213532_c3_351	2813	6585	246	81	90	0.00022

Description

gp: [GI:g208931] [LN:SYNORFLAC] [AC:M15619] [OR:synthetic construct] [SR:E.coli (strain SE5000) synthetic DNA, clone pKB1] [DB:genpept-syn] [DE:Synthetic E.coli ORF16/lacZ fusion protein, partial cds.] [NT:ORF16-lacZ fusion protein] [LE:29] [RE:>232] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000998_1178785_c3_323	2814	6586	939	312	731	2.6e-72

Description

pir: [LN:H69973] [AC:H69973] [PN:cysteine synthase homolog yrhA] [GN:yrhA] [CL:threonine dehydratase] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:g1934605] [LN:BSU93874] [AC:U93874] [PN:cysteine synthase] [GN:yrhA] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis cysteine synthase (yrhA), cystathioninegamma-lyase (yrhB), YrhC (yrhC), YrhD (yrhD), formate dehydrogenasechain A (yrhE), YrhF (yrhF), formate dehydrogenase (yrhG), YrhH(yrhH), regulatory protein (yrhI), cytochrome P450 102 (yrhJ), YrhK(yrhK), hypothetical protein YrhL (yrhL), putative anti-SigV factor(yrhM), RNA polymerase sigma factor SigV (sigV) and YrhO (yrhO)genes, complete cds, and YrhP (yrhP) gene, partial cds.] [NT:similar to cysteine synthase from Spinacia] [LE:61] [RE:984] [DI:direct] >gp: [GI:e1183956:g2635172] [LN:BSUB0014] [AC:Z99117:AL009126] [GN:yrhA] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.] [NT:similar to cysteine synthase] [LE:185962] [RE:186885] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000998_11931540_f2_96	2815	6587	825	274	786	3.8e-78

Description

sp: [LN:YLAC\_STAXY] [AC:O33812] [OR:STAPHYLOCOCCUS XYLOSUS] [DE:HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN LACR 5'REGION (FRAGMENT)] [SP:O33812] [DB:swissprot] >gp: [GI:e352090:g2462703] [LN:SXLACRPH] [AC:Y14599] [PN:transcriptional regulator from the LysR-type] [OR:Staphylococcus xylosus] [DB:genpept-bct1] [DE:Staphylococcus xylosus lacR, lacP, lacH genes and 2 ORF's.] [NT:ORF1] [SP:O33812] [LE:<1] [RE:814] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000998_1256387_c2_297	2816	6588	129	42		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000998_12603166_f2_86	2817	6589	303	100	100	1.9e-05

Description

pir: [LN:G71244] [AC:G71244] [PN:hypothetical protein PH0217] [GN:PH0217] [OR:Pyrococcus horikoshii] [DB:pir2] >gp: [GI:d1030229:g3256603] [LN:AP000001] [AC:AP000001:AB009465:AB009464:AB009466:AB009467:AB009468:AB009469] [PN:106aa long hypothetical protein] [GN:PH0217] [OR:Pyrococcus horikoshii] [SR:Pyrococcus horikoshii (strain:OT3) DNA] [DB:genpept-bct1] [DE:Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt. position (1/7).] [LE:191072] [RE:191392] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000998_126068_f1_46	2818	6590	555	184	164	3.4e-11

Description

pir: [LN:A71661] [AC:A71661] [PN:hypothetical protein RP563] [GN:RP563] [OR:Rickettsia prowazekii] [DB:pir2] >gp: [GI:e1342855:g3861111] [LN:RPXX03] [AC:AJ235272:AJ235269] [PN:unknown] [GN:RP563] [OR:Rickettsia prowazekii] [DB:genpept-bct1] [DE:Rickettsia prowazekii strain Madrid E, complete genome; segment3/4.] [LE:110476] [RE:112242] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000998_13089052_f3_214	2819	6591	123	40		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000998_13678300_c2_267	2820	6592	1233	410	1393	1.8e-142

Description

pir: [LN:B69760] [AC:B69760] [PN:conserved hypothetical protein yciC] [GN:yciC] [CL:conserved hypothetical protein yciC] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1182288:g2632622] [LN:BSUB0002] [AC:Z99105:AL009126] [GN:yciC] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 2 of 21): from 194651 to 415810.] [NT:similar to hypothetical proteins] [LE:170984] [RE:172177] [DI:direct] >gp: [GI:d1009605:g1805408] [LN:D50453] [AC:D50453] [PN:homologues to nitrile hydratase region] [GN:yciC] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:168 trpC2) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis DNA for 25-36 degree region containing theamyE-srfA region, complete cds.] [LE:45287] [RE:46480] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503000998_13912712_c3_312	2821	6593	150	49	52	0.015
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Description

sp: [LN:IMM1\_ECOLI] [AC:P02985] [GN:IMM] [OR:ESCHERICHIA COLI] [DE:COLICIN E1 IMMUNITY PROTEIN (IMME1) (MICROGIN E1 IMMUNITY PROTEIN)] [SP:P02985] [DB:swissprot] >gp: [GI:g455140] [LN:CE1CEA] [AC:M12543] [OR:Plasmid ColE1] [SR:Plasmid ColE1 (a colicin-producing derivative strain from E.coli) [DB:genpept-bct1] [DE:Plasmid ColE1 cea (3' end), imm and lys genes (complete cds).] [NT:immunity protein] [LE:32] [RE:373] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503000998_13923427_f3_196	2822	6594	135	44		
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503000998_14218805_c2_301	2823	6595	129	42	80	0.0095
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Description

sp: [LN:TRER\_BACSU] [AC:P39796] [GN:TRER] [OR:BACILLUS SUBTILIS] [DE:TREHALOSE OPERON TRANSCRIPTIONAL REPRESSOR] [SP:P39796] [DB:swissprot] >pir: [LN:JC5038] [AC:JC5038:S67931:D69725:I40499:S67866] [PN:transcription repressor of trehalose operon treR] [GN:treR] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:g1000453] [LN:BSTREAPR] [AC:Z54245] [PN:TreR] [GN:treR] [FN:repressor of the trehalose operon] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis treA, treP and treR genes.] [NT:position 3684 corresponds to position 2543 of] [SP:P39796] [LE:3352] [RE:4068] [DI:direct] >gp: [GI:e1182772:g2633106] [LN:BSUB0005] [AC:Z99108:AL009126] [PN:transcriptional regulator (GntR family)] [GN:treR] [FN:negative regulation of the trehalose operon] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 5 of 21): from 802821 to 1011250.] [NT:alternate gene name: yfxA] [SP:P39796] [LE:50243] [RE:50959] [DI:direct] >gp: [GI:d1024286:g2626829] [LN:D83967] [AC:D83967] [PN:TreR] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:AC327) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis genomic DNA, 74 degree region.] [LE:16962] [RE:17678] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503000998_14271068_f1_51	2824	6596	261	86	68	0.018
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Description

sp: [LN:PROP\_ECOLI] [AC:P30848] [GN:PROP] [OR:ESCHERICHIA COLI] [DE:PROLINE/BETAINE TRANSPORTER (PROLINE PORTER II) (PPII)] [SP:P30848] [DB:swissprot] >pir: [LN:S32331] [AC:S32331:S56339:F65220] [PN:proline/betaine transport protein:proline permease II:proline porter II] [GN:proP] [CL:citrate utilization determinant] [OR:Escherichia coli] [DB:pir2] [MP:93 min] >gp: [GI:g147357] [LN:ECOPROBETT] [AC:M83089] [PN:a proline/betaine transporter] [GN:proP] [FN:active uptake of proline or betaine] [OR:Escherichia coli] [DB:genpept-bct1] [DE:E. coli proline/betaine transporter (proP) gene, complete cds.] [NT:Evidence that this open reading frame encodes a] [LE:433] [RE:1935] [DI:direct] >gp: [GI:g536955] [LN:ECOUW93] [AC:U14003] [GN:proP] [FN:active uptake of proline or betaine] [OR:Escherichia coli] [DB:genpept-bct1] [DE:Escherichia coli K-12 chromosomal region from 92.8 to 00.1 minutes.] [NT:CG Site No. 361] [LE:21331] [RE:22833] [DI:direct] >gp: [GI:g1790550] [LN:AE000483] [AC:AE000483:U00096] [PN:low-affinity transport system; proline permease] [GN:proP] [FN:transport; Transport of small molecules: Amino] [OR:Escherichia coli] [DB:genpept-bct2] [DE:Escherichia coli K-12 MG1655 section 373 of 400 of the complete genome.] [NT:o500; 100 pct identical to PROP\_ECOLI SW: P30848;] [LE:5301] [RE:6803] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000998_14460882_c1_217	2825	6597	1695	564	1304	4.9e-133

Description

gp: [GI:g1022726] [LN:SHU35635] [AC:U35635] [PN:unknown] [OR:Staphylococcus haemolyticus] [SR:Staphylococcus haemolyticus strain=Y176] [DB:genpept-bct1] [DE:Staphylococcus haemolyticus IS1272 ORF1 and ORF2 genes, completecds.] [NT:ORF1] [LE:1101] [RE:1922] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000998_14485686_c2_287	2826	6598	153	50		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000998_15022153_f1_73	2827	6599	189	62		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000998_15900305_f3_177	2828	6600	789	262	78	0.019

Description

gp: [GI:g453517] [LN:TETRRTRNA] [AC:L28677] [OR:Mitochondrion Tetrahymena pyriformis] [SR:Mitochondrion Tetrahymena pyriformis (strain ST, organell] [DB:genpept-inv1] [DE:Tetrahymena pyriformis ribosomal RNA; tRNA-Trp; ORF 1-4; tRNA-Glu; cytochrome oxidase subunit 1; NADH dehydrogenase; ribosomal proteinL14.] [NT:ORF3] [LE:4384] [RE:4680] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000998_16196963_f2_133	2829	6601	192	63		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000998_16257665_f1_37	2830	6602	192	63		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000998_16281286_c3_322	2831	6603	1359	452	1059	4.5e-107

Description

pir: [LN:F69825] [AC:F69825] [PN:sodium-dependent transporter homolog yhdH] [GN:yhdH] [CL:gamma-aminobutyric acid transporter] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1182948:g2633282] [LN:BSUB0006] [AC:Z99109:AL009126] [GN:yhdH] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 6 of 21): from 999501 to 1209940.] [NT:similar to sodium-dependent transporter] [LE:24845] [RE:26200] [DI:direct] >gp: [GI:e1191879:g2226203] [LN:BSY14082] [AC:Y14082] [PN:hypothetical protein] [GN:yhdH] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis chromosomal DNA, region 72 to 75 degrees: spoVRto sspB.] [NT:Similarity to sodium dependent transporters;] [LE:11493] [RE:12848] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000998_19712762_c3_347	2832	6604	600	199	813	5.2e-81

Description

sp: [LN:RECR\_BACSU] [AC:P24277] [GN:RECR:RECM:RECD] [OR:BACILLUS SUBTILIS] [DE:RECOMBINATION PROTEIN RECR] [SP:P24277] [DB:swissprot] >pir: [LN:B69691] [AC:B69691:S13788:S66051] [PN:DNA repair and genetic recombination recR:recM protein] [GN:recR] [CL:recR protein] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:d1005799:g467411] [LN:BAC180K] [AC:D26185] [PN:recombination protein] [GN:recR] [OR:Bacillus subtilis] [SR:Bacillus subtilis (sub\_species:Marburg, strain:168) DNA] [DB:genpept-bct1] [DE:B. subtilis DNA, 180 kilobase region of replication origin.] [LE:92467] [RE:93063] [DI:direct] >gp: [GI:g453239] [LN:BSRECM] [AC:X17014] [GN:recR] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis dnaZX and recR genes and two unidentified readingframes.] [SP:P24277] [LE:2314] [RE:2910] [DI:direct] >gp: [GI:e1181954:g2632288] [LN:BSUB0001] [AC:Z99104:AL009126] [GN:recR] [FN:DNA repair and genetic recombination] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 1 of 21): from 1 to 213080.] [NT:alternate gene name: recM] [SP:P24277] [LE:28865] [RE:29461] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000998_19960162_c1_232	2833	6605	2631	876	1785	5.2e-184

Description

pir: [LN:E69745] [AC:E69745] [PN:hypothetical protein ybcD] [GN:ybcD] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1182118:g2632452] [LN:BSUB0001] [AC:Z99104:AL009126] [GN:ybcD] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 1 of 21): from 1 to 213080.] [LE:207166] [RE:209430] [DI:direct] >gp: [GI:e1182136:g2632470] [LN:BSUB0002] [AC:Z99105:AL009126] [GN:ybcD] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 2 of 21): from 194651 to 415810.] [LE:12516] [RE:14780] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000998_20093_c3_311	2834	6606	306	101		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000998_20314005_c3_335	2835	6607	4590	1529	4186	0.0

Description

sp: [LN:GLTB\_BACSU] [AC:P39812] [GN:GLTB:GLTA] [OR:BACILLUS SUBTILIS] [EC:1.4.1.13] [DE:GLUTAMATE SYNTHASE [NADPH] LARGE CHAIN, (NADPH-GOGAT)] [SP:P39812] [DB:swissprot] >pir: [LN:G69634] [AC:G69634] [PN:glutamate synthase (large subunit) gltA] [GN:gltA] [CL:glutamate synthase (NADPH)] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1183503:g2634228] [LN:BSUB0010] [AC:Z99113:AL009126] [PN:glutamate synthase (large subunit)] [GN:gltA] [FN:glutamate biosynthesis] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:1.4.1.13] [DE:Bacillus subtilis complete genome (section 10 of 21): from 1781201 to 2014980.] [SP:P39812] [LE:228126] [RE:232688] [DI:complement] >gp: [GI:e1185318:g2634239] [LN:BSUB0011] [AC:Z99114:AL009126] [PN:glutamate synthase (large subunit)] [GN:gltA] [FN:glutamate biosynthesis] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:1.4.1.13] [DE:Bacillus subtilis complete genome (section 11 of 21): from 2000171 to 2207900.] [SP:P39812] [LE:9156] [RE:13718] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000998_203886_f2_137	2836	6608	159	52	116	2.8e-06

Description

gp: [GI:g2689564] [LN:U93688] [AC:U93688] [PN:integrase] [GN:int] [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus toxic shock syndrome toxin-1 (tst), enterotoxin (ent), and integrase (int) genes, complete cds.] [NT:similar to staphylococcal phage integrase] [LE:13871] [RE:15091] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000998_20602262_c2_303	2837	6609	543	180	105	0.00015
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Description

sp: [LN:YHBS\_ECOLI] [AC:P45473] [GN:YHBS] [OR:ESCHERICHIA COLI] [DE:HYPOTHETICAL 18.5 KD PROTEIN IN SOHA-MTR INTERGENIC REGION (F167)] [SP:P45473] [DB:swissprot]  
 >pir: [LN:H65105] [AC:H65105] [PN:hypothetical protein b3156] [OR:Escherichia coli] [DB:pir2] >gp: [GI:g606096] [LN:ECOUW67] [AC:U18997] [OR:Escherichia coli] [DB:genpept-bct1] [DE:Escherichia coli K-12 chromosomal region from 67.4 to 76.0 minutes.] [NT:ORF\_f167; end overlaps end of o100 by 14 bases;] [LE:81007] [RE:81510] [DI:complement] >gp: [GI:g1789546] [LN:AE000396] [AC:AE000396:U00096] [PN:orf, hypothetical protein] [GN:yhbS] [FN:orf; Unknown] [OR:Escherichia coli] [DB:genpept-bct2] [DE:Escherichia coli K-12 MG1655 section 286 of 400 of the complete genome.] [NT:f167; f167; end overlaps end of o100 by 14] [LE:6918] [RE:7421] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000998_20602263_c2_270	2838	6610	1512	503	1414	1.1e-144
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Description

sp: [LN:NDHF\_BACSU] [AC:P39755] [GN:NDHF] [OR:BACILLUS SUBTILIS] [EC:1.6.5.3] [DE:OXIDOREDUCTASE CHAIN 5] [SP:P39755] [DB:swissprot] >pir: [LN:C69666] [AC:C69666] [PN:NADH dehydrogenase (subunit 5) ndhF] [GN:ndhF] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:d1034042:g3599601] [LN:AB006424] [AC:AB006424] [PN:NADH DEHYDROGENASE SUBUNIT 5] [GN:ndhF] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:168) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis genomic DNA, 70 kb region between 17 and 23degree.] [LE:8378] [RE:9895] [DI:direct] >gp: [GI:g903587] [LN:BSU28323] [AC:U28323] [PN:NADH dehydrogenase subunit 5] [GN:ndhF] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis NADH dehydrogenase subunit 5 (ndhF) gene, complete cds.] [LE:519] [RE:2036] [DI:direct] >gp: [GI:e1182116:g2632450] [LN:BSUB0001] [AC:Z99104:AL009126] [PN:NADH dehydrogenase (subunit 5)] [GN:ndhF] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:1.6.5.3] [DE:Bacillus subtilis complete genome (section 1 of 21): from 1 to 213080.] [NT:alternate gene name: ybxE] [SP:P39755] [LE:205395] [RE:206912] [DI:direct] >gp: [GI:e1182134:g2632468] [LN:BSUB0002] [AC:Z99105:AL009126] [PN:NADH dehydrogenase (subunit 5)] [GN:ndhF] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:1.6.5.3] [DE:Bacillus subtilis complete genome (section 2 of 21): from 194651 to 415810.] [NT:alternate gene name: ybxE] [SP:P39755] [LE:10745] [RE:12262] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000998_2142316_f3_207	2839	6611	213	70	52	0.040
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Description

gp: [GI:e1287275:g3063696] [LN:ATF4D11] [AC:AL022537] [PN:putative protein] [GN:F4D11.60] [OR:Arabidopsis thaliana] [SR:thale cress] [DB:genpept-pln1] [DE:Arabidopsis thaliana DNA chromosome 4, BAC clone F4D11 (ESSAI project).] [NT:contains EST gb:W43721] [LE:21418:21729:22060] [RE:21537:22004:22174] [DI:complementJoin]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000998_21516287_f1_2	2840	6612	126	41		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000998_2195338_c3_342	2841	6613	165	54		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000998_22305342_f3_205	2842	6614	543	180	162	8.7e-11

Description

gp: [GI:g4019275] [LN:AF083424] [AC:AF083424] [OR:Ateline herpesvirus 3]  
 [DB:genpept-vrl] [DE:Ateline herpesvirus 3 complete genome.] [NT:orf 48] [LE:62159]  
 [RE:64537] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000998_22437751_c3_307	2843	6615	489	162	160	5.5e-11

Description

pir: [LN:T03492] [AC:T03492] [PN:hypothetical protein] [OR:Rhodobacter capsulatus]  
 [DB:pir2] [MP:1] >gp: [GI:g3128293] [LN:AF010496] [AC:AF010496] [PN:hypothetical  
 protein] [OR:Rhodobacter capsulatus] [DB:genpept-bct2] [DE:Rhodobacter capsulatus  
 strain SB1003, partial genome.] [LE:54291] [RE:55613] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000998_22459802_f2_135	2844	6616	156	51	117	1.0e-06

Description

gp: [GI:g1022726] [LN:SHU35635] [AC:U35635] [PN:unknown] [OR:Staphylococcus  
 haemolyticus] [SR:Staphylococcus haemolyticus strain=Y176] [DB:genpept-bct1]  
 [DE:Staphylococcus haemolyticus IS1272 ORF1 and ORF2 genes, completecds.] [NT:ORF1]  
 [LE:1101] [RE:1922] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000998_22688428_c3_348	2845	6617	144	47		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000998_23484678_c2_304	2846	6618	1731	576	1263	1.1e-128

Description

pir: [LN:S13786] [AC:S13786:S00745:S66049:B69618] [PN:DNA-directed DNA polymerase, III chain dnaX:DNA polymerase III (gamma and tau subunits) dnaX] [GN:dnax:dnazx] [OR:Bacillus subtilis] [EC:2.7.7.7] [DB:pir2] >gp: [GI:d1005797:g467409] [LN:BAC180K] [AC:D26185] [PN:DNA polymerase III subunit] [GN:dnah] [OR:Bacillus subtilis] [SR:Bacillus subtilis (sub\_species:Marburg, strain:168) DNA] [DB:genpept-bct1] [DE:B. subtilis DNA, 180 kilobase region of replication origin.] [LE:90414] [RE:92105] [DI:direct] >gp: [GI:g580914] [LN:BSRECM] [AC:X17014] [GN:dnazx] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis dnaZX and recR genes and two unidentified readingframes.] [SP:P09122] [LE:261] [RE:1952] >gp: [GI:e1181952:g2632286] [LN:BSUB0001] [AC:Z99104:AL009126] [PN:DNA polymerase III (gamma and tau subunits)] [GN:dnax] [FN:DNA synthesis] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:2.7.7.7] [DE:Bacillus subtilis complete genome (section 1 of 21): from 1 to 213080.] [NT:alternate gene name: dnah, dna-8132] [SP:P09122] [LE:26812] [RE:28503] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000998_23556500_f1_33	2847	6619	282	93		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000998_2359675_c3_329	2848	6620	141	46	68	0.047

Description

pir: [LN:S72295] [AC:S72295] [PN:ribosomal protein S8] [GN:rps8] [OR:plastid Plasmodium falciparum] [DB:pir2] >gp: [GI:e220199:g1171601] [LN:PFCOMPIRB] [AC:X95276] [GN:rps8] [OR:Plasmodium falciparum] [SR:malaria parasite P. falciparum] [DB:genpept-inv1] [DE:P. falciparum complete gene map of plastid-like DNA (IR-B).] [LE:5492] [RE:5878] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000998_23631262_f2_94	2849	6621	150	49		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000998_23994687_f1_45	2850	6622	132	43		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000998_24016916_c3_341	2851	6623	1044	347	396	8.1e-37
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Description

sp: [LN:YEIH\_ECOLI] [AC:P33019] [GN:YEIH] [OR:ESCHERICHIA COLI] [DE:HYPOTHETICAL 36.9 KD PROTEIN IN LYSP-NFO INTERGENIC REGION] [SP:P33019] [DB:swissprot] >pir: [LN:E64984] [AC:E64984] [PN:hypothetical 36.9 kD protein in lysP-nfo intergenic region] [GN:yeiH] [OR:Escherichia coli] [DB:pir2] >gp: [GI:g405879] [LN:ECOHU47] [AC:U00007] [PN:yeiH] [OR:Escherichia coli] [SR:Escherichia coli K12 BHB2600] [DB:genpept-bct1] [DE:47 to 48 centisome region of E.coli K12 BHB2600.] [LE:57462] [RE:58511] [DI:direct] >gp: [GI:g1788482] [LN:AE000305] [AC:AE000305:U00096] [PN:orf, hypothetical protein] [GN:yeiH] [FN:orf; Unknown] [OR:Escherichia coli] [DB:genpept-bct2] [DE:Escherichia coli K-12 MG1655 section 195 of 400 of the complete genome.] [NT:o349; 100 pct identical to YEIH\_ECOLI SW: P33019] [LE:2831] [RE:3880] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000998_24220967_c1_228	2852	6624	138	45		
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000998_24227192_c3_343	2853	6625	147	48		
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000998_24235626_c1_257	2854	6626	159	52		
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000998_24272337_f3_204	2855	6627	432	143	96	0.0025
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Description

pir: [LN:D69633] [AC:D69633] [PN:glutamine ABC transporter (glutamine-binding protein glnH)] [GN:glnH] [CL:lysine-arginine-ornithine-binding protein] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1183973:g2635189] [LN:BSUB0014] [AC:Z99117:AL009126] [PN:glutamine ABC transporter (glutamine-binding)] [GN:glnH] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 14 of 21): from 2599451 to 2812870.] [LE:202928] [RE:203749] [DI:direct] >gp: [GI:e1183991:g2635207] [LN:BSUB0015] [AC:Z99118:AL009126] [PN:glutamine ABC transporter (glutamine-binding)] [GN:glnH] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 15 of 21): from 2795131 to 3013540.] [LE:7248] [RE:8069] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000998_24350953_f1_6	2856	6628	132	43	72	0.017
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Description

pir: [LN:G71244] [AC:G71244] [PN:hypothetical protein PH0217] [GN:PH0217] [OR:Pyrococcus horikoshii] [DB:pir2] >gp: [GI:d1030229:g3256603] [LN:AP000001] [AC:AP000001:AB009465:AB009464:AB009466:AB009467:AB009468:AB009469] [PN:106aa long hypothetical protein] [GN:PH0217] [OR:Pyrococcus horikoshii] [SR:Pyrococcus horikoshii (strain:OT3) DNA] [DB:genpept-bct1] [DE:Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt. position (1/7).] [LE:191072] [RE:191392] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000998_24390937_f3_198	2857	6629	156	51		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000998_24391885_f3_178	2858	6630	183	60		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000998_24475252_f3_213	2859	6631	159	52		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000998_24664802_c1_234	2860	6632	747	248	380	4.0e-35

Description

pir: [LN:H70027] [AC:H70027] [PN:carboxylesterase homolog yvaK] [GN:yvaK] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1186050:g2635875] [LN:BSUB0018] [AC:Z99121:AL009126] [GN:yvaK] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 18 of 21): from 3399551 to 3609060.] [NT:similar to carboxylesterase] [LE:53733] [RE:54479] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000998_25422288_c2_277	2861	6633	153	50		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000998_25442803_c2_306	2862	6634	261	86		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000998_25586693_c3_346	2863	6635	333	110	374	1.7e-34

Description

sp: [LN:YAAK\_BACSU] [AC:P24281] [GN:YAAK] [OR:BACILLUS SUBTILIS] [DE:HYPOTHETICAL 11.8 KD PROTEIN IN DNAZ-RECR INTERGENIC REGION] [SP:P24281] [DB:swissprot] >pir: [LN:S13787] [AC:S13787:S66050:C69737] [PN:conserved hypothetical protein yaaK] [GN:yaaK] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:d1005798:g467410] [LN:BAC180K] [AC:D26185] [PN:unknown] [OR:Bacillus subtilis] [SR:Bacillus subtilis (sub\_species:Marburg, strain:168) DNA] [DB:genpept-bct1] [DE:B. subtilis DNA, 180 kilobase region of replication origin.] [LE:92129] [RE:92452] [DI:direct] >gp: [GI:g40073] [LN:BSRECM] [AC:X17014] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis dnaZX and recR genes and two unidentified readingframes.] [NT:ORF107] [SP:P24281] [LE:1976] [RE:2299] [DI:direct] >gp: [GI:e1181953:g2632287] [LN:BSUB0001] [AC:Z99104:AL009126] [GN:yaaK] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 1 of 21): from 1 to 213080.] [NT:similar to hypothetical proteins] [SP:P24281] [LE:28527] [RE:28850] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503000998_256468_c2_294	2864	6636	330	109		
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503000998_26460887_f1_34	2865	6637	1524	507	366	6.4e-32
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Description

sp: [LN:TAGE\_BACSU] [AC:P13484] [GN:TAGE:RODD:GTAA] [OR:BACILLUS SUBTILIS] [EC:2.4.1.52] [DE:(EC 2.4.1.52) (TEICHOIC ACID BIOSYNTHESIS PROTEIN E)] [SP:P13484] [DB:swissprot] >pir: [LN:S06048] [AC:S06048:F69720] [PN:poly(glycerol-phosphate) alpha-glucosyltransferase, tagE:probable rodD protein:UDP-glucose--polyglycerol phosphate glucosyltransferase tagE] [GN:tagE:rodD] [OR:Bacillus subtilis] [EC:2.4.1.52] [DB:pir2] [MP:310 degrees] >gp: [GI:g580920] [LN:BSRODC] [AC:X15200] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis rodC operon.] [NT:rodD (gtaA) polypeptide (AA 1-673)] [SP:P13484] [LE:157] [RE:2178] [DI:direct] >gp: [GI:e1184479:g2636099] [LN:BSUB0019] [AC:Z99122:AL009126] [PN:UDP-glucose:polyglycerol phosphate] [GN:tagE] [FN:teichoic acid biosynthesis] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:2.4.1.52] [DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091 to 3809700.] [NT:alternate gene name: rodD, gtaA, gtaD] [SP:P13484] [LE:80369] [RE:82390] [DI:complement] >gp: [GI:e1184479:g2636099] [LN:BSUB0019] [AC:Z99122:AL009126] [PN:UDP-glucose:polyglycerol phosphate] [GN:tagE] [FN:teichoic acid biosynthesis] [OR:Bacillus subtilis] [DB:genpept] [EC:2.4.1.52] [DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091 to 3809700.] [NT:alternate gene name: rodD, gtaA, gtaD] [SP:P13484] [LE:80369] [RE:82390] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503000998_26776562_c3_317	2866	6638	399	132		
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503000998_2769816_f3_206	2867	6639	135	44	135	2.5e-08
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Description

gp: [GI:g2689564] [LN:U93688] [AC:U93688] [PN:integrase] [GN:int] [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus toxic shock syndrome toxin-1 (tst), enterotoxin (ent), and integrase (int) genes, complete cds.] [NT:similar to staphylococcal phage integrase] [LE:13871] [RE:15091] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503000998_30265952_c2_291	2868	6640	387	128	118	2.3e-07
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Description

pir: [LN:H69029] [AC:H69029] [PN:mutator MutT related protein] [GN:MTH122] [CL:mutT domain homology] [OR:Methanobacterium thermoautotrophicum] [DB:pir2] >gp: [GI:g2621161] [LN:AE000801] [AC:AE000801:AE000666] [PN:mutator MutT related protein] [GN:MTH122] [OR:Methanobacterium thermoautotrophicum] [DB:genpept-bct1] [DE:Methanobacterium thermoautotrophicum from bases 68653 to 79584(section 7 of 148) of the complete genome.] [NT:Function Code:10.09 - Metabolism of Macromolecules,] [LE:9193] [RE:9660] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000998_30682802_c3_321	2869	6641	261	86		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000998_33399055_c2_273	2870	6642	393	130	419	3.0e-39

Description

pir:[LN:H69745] [AC:H69745] [PN:hypothetical protein ybcI] [GN:ybcI] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:d1034047:g3599606] [LN:AB006424] [AC:AB006424] [GN:ybcI] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:168) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis genomic DNA, 70 kb region between 17 and 23degree.] [LE:13549] [RE:13923] [DI:direct] >gp:[GI:e1182121:g2632455] [LN:BSUB0001] [AC:Z99104:AL009126] [GN:ybcI] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 1 of 21): from 1 to 213080.] [LE:210558] [RE:210932] [DI:direct] >gp:[GI:e1182139:g2632473] [LN:BSUB0002] [AC:Z99105:AL009126] [GN:ybcI] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 2 of 21): from 194651 to 415810.] [LE:15908] [RE:16282] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000998_33756432_f1_7	2871	6643	141	46		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000998_34407625_c3_309	2872	6644	354	117	587	4.7e-57

Description

gp:[GI:g1658281] [LN:SLU74623] [AC:U74623] [PN:CadX] [FN:cadmium resistance] [OR:Staphylococcus lugdunensis] [DB:genpept-bct1] [DE:Staphylococcus lugdunensis strain 995 cadmium resistance plasmid pLUG10, complete sequence.] [LE:2624] [RE:2971] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000998_34557262_c3_349	2873	6645	135	44		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000998_35431657_f2_114	2874	6646	135	44		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000998_36227142_c1_240	2875	6647	993	330	409	3.4e-38

Description

sp: [LN:LYTE\_BACSU] [AC:P54421] [GN:LYTE:PAPQ] [OR:BACILLUS SUBTILIS] [DE:PAPQ PRECURSOR) (CELL WALL-ASSOCIATED POLYPEPTIDE CWBP33)] [SP:P54421] [DB:swissprot] >gp: [GI:g1488662] [LN:BSU38819] [AC:U38819] [PN:phosphatase-associated protein] [GN:lytE] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis phosphatase-associated protein (lytE) gene, complete cds.] [NT:Muralytic when cloned in E.coli; Iap60 homolog;] [LE:443] [RE:1447] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000998_36568828_c2_266	2876	6648	1050	349	984	4.0e-99

Description

pir: [LN:A43577] [AC:A43577] [PN:regulatory protein pfoR] [OR:Clostridium perfringens] [DB:pir2]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000998_36593802_c2_282	2877	6649	867	288	454	5.8e-43

Description

sp: [LN:PLPA\_PASHA] [AC:Q08868:Q07363] [GN:PLPA] [OR:PASTURELLA HAEMOLYTICA] [DE:OUTER MEMBRANE LIPOPROTEIN 1 PRECURSOR (PLP1)] [SP:Q08868:Q07363] [DB:swissprot] >pir: [LN:JN0751] [AC:JN0751] [PN:Outer membrane 30K protein:ORF1] [CL:lipoprotein-28] [OR:Pasteurella haemolytica] [DB:pir2] >gp: [GI:g349530] [LN:PASLIOPR] [AC:L11037] [PN:lipoprotein] [OR:Pasteurella haemolytica] [SR:Pasteurella haemolytica (strain A1) DNA] [DB:genpept-bct1] [DE:Pasteurella haemolytica lipoprotein gene, complete cds.] [NT:precursor] [LE:171] [RE:1004] [DI:direct] >gp: [GI:g150508] [LN:PASLIOPRO] [AC:M91072] [PN:lipoprotein] [OR:Pasteurella haemolytica] [SR:Pasteurella haemolytica (strain A1) (library: pUC19 of R. Craven e] [DB:genpept-bct1] [DE:Pasteurella haemolytica (clones pGEB2830,pBRES2830) lipoproteingene, complete cds.] [LE:136] [RE:969] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000998_3944143_c3_308	2878	6650	627	208	971	9.5e-98

Description

gp: [GI:g1916729] [LN:AF134905] [AC:AF134905:U76550] [PN:CadD] [GN:cadD] [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus plasmid pRW001 CadD (cadD) gene, completecds.] [NT:confers low level cadmium resistance] [LE:2328] [RE:2957] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000998_3945253_f3_203	2879	6651	126	41		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000998_3954385_f1_32	2880	6652	123	40		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000998_4064818_c1_239	2881	6653	675	224	533	2.5e-51

Description

sp: [LN:YAAE\_ECOLI] [AC:P31547] [GN:YAAE] [OR:ESCHERICHIA COLI] [DE:HYPOTHETICAL ABC TRANSPORTER PERMEASE PROTEIN YAAE] [SP:P31547] [DB:swissprot] >pir: [LN:F64744] [AC:F64744] [PN:probable transport protein yaeE] [GN:yaeE] [CL:probable transport protein yaeE] [OR:Escherichia coli] [DB:pir2] >gp: [GI:d1041643:g4902941] [LN:ECOTSF] [AC:D83536] [PN:Hypothetical 23.3 kd protein in rcsF-abc] [GN:yaeE] [OR:Escherichia coli] [SR:Escherichia coli (strain:K12) DNA] [DB:genpept-bct1] [DE:Escherichia coli genomic DNA. (4.1 - 6.1 min.)] [NT:ORF\_ID:o124#1; similar to SwissProt Accession] [LE:30521] [RE:31174] [DI:complement] >gp: [GI:g1552774] [LN:ECU70214] [AC:U70214] [GN:yaeE] [OR:Escherichia coli] [DB:genpept-bct1] [DE:Escherichia coli chromosome minutes 4-6.] [NT:hypothetical] [LE:52043] [RE:52696] [DI:complement] >gp: [GI:g1786397] [LN:AE000129] [AC:AE000129:U00096] [PN:putative transport system permease protein] [GN:yaeE] [FN:putative transport; Not classified] [OR:Escherichia coli] [DB:genpept-bct2] [DE:Escherichia coli K-12 MG1655 section 19 of 400 of the complete genome.] [NT:f218; 100 pct identical to YAAE\_ECOLI SW: P31547] [LE:944] [RE:1597] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000998_4082828_c3_320	2882	6654	702	233	211	3.3e-17

Description

pir: [LN:F71886] [AC:F71886] [PN:hypothetical protein jhp0787] [GN:jhp0787] [OR:Helicobacter pylori] [SR:strain J99, , strain J99] [SR:strain J99, ] [DB:pir2] >gp: [GI:g4155367] [LN:AE001509] [AC:AE001509:AE001439] [PN:putative] [GN:jhp0787] [OR:Helicobacter pylori J99] [DB:genpept-bct2] [DE:Helicobacter pylori, strain J99 section 70 of 132 of the complete genome.] [NT:similar to H. pylori 26695 gene HP0851] [LE:2708] [RE:3394] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000998_4101525_f1_60	2883	6655	135	44		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000998_4328468_c2_298	2884	6656	1473	490	1279	2.2e-130

Description

pir: [LN:H69634] [AC:H69634] [PN:glutamate synthase (small subunit) gltB] [GN:gltB] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1183502:g2634227] [LN:BSUB0010] [AC:Z99113:AL009126] [PN:glutamate synthase (small subunit)] [GN:gltB] [FN:glutamate biosynthesis] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:1.4.1.13] [DE:Bacillus subtilis complete genome (section 10 of 21): from 1781201 to 2014980.] [LE:226628] [RE:228109] [DI:complement] >gp: [GI:e1185317:g2634238] [LN:BSUB0011] [AC:Z99114:AL009126] [PN:glutamate synthase (small subunit)] [GN:gltB] [FN:glutamate biosynthesis] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:1.4.1.13] [DE:Bacillus subtilis complete genome (section 11 of 21): from 2000171 to 2207900.] [LE:7658] [RE:9139] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000998_4335766_c1_261	2885	6657	141	46		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503000998_4344011_f3_152	2886	6658	252	83	60	0.023
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Description

gp: [GI:d1036760:g4062561] [LN:D90737] [AC:D90737:AB001340] [PN:4-hydroxyphenylacetate 3-monooxygenase (EC) [GN:nmoB] [OR:Escherichia coli] [SR:Escherichia coli(strain:K12) DNA, clone:Kohara clone #227] [DB:genpept-bct1] [DE:Escherichia coli genomic DNA. (22.8 - 23.1 min).] [NT:ORF\_ID:o228#5; similar to PIR Accession Number] [LE:15357] [RE:15932] [DI:complement] >gp: [GI:d1036770:g4062570] [LN:D90738] [AC:D90738:AB001340] [PN:4-hydroxyphenylacetate 3-monooxygenase (EC) [GN:nmoB] [OR:Escherichia coli] [SR:Escherichia coli(strain:K12) DNA, clone:Kohara clone #228] [DB:genpept-bct1] [DE:Escherichia coli genomic DNA. (23.0 - 23.4 min).] [NT:ORF\_ID:o228#5; similar to PIR Accession Number] [LE:3821] [RE:4396] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503000998_4485682_f3_159	2887	6659	264	87		
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503000998_4580132_f1_72	2888	6660	171	56	161	3.6e-11
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Description

gp: [GI:g2689564] [LN:U93688] [AC:U93688] [PN:integrase] [GN:int] [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus toxic shock syndrome toxin-1 (tst), enterotoxin (ent), and integrase (int) genes, complete cds.] [NT:similar to staphylococcal phage integrase] [LE:13871] [RE:15091] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503000998_4703167_f1_44	2889	6661	144	47		
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503000998_4703512_c3_315	2890	6662	486	161	335	2.4e-30
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Description

pir: [LN:A70068] [AC:A70068] [PN:conserved hypothetical protein ywqN] [GN:ywqN] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1184521:g2636140] [LN:BSUB0019] [AC:Z99122:AL009126] [GN:ywqN] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.] [NT:similar to hypothetical proteins] [LE:124753] [RE:125298] [DI:complement] >gp: [GI:e308071:g1894752] [LN:BSZ92952] [AC:Z92952] [PN:unknown] [GN:ywqN] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B. subtilis ywq[A,B,C,D,E,F,G,H,I,J,K,L,M,N,O] genes.] [LE:13028] [RE:13573] [DI:direct] >gp: [GI:e1184521:g2636140] [LN:BSUB0019] [AC:Z99122:AL009126] [GN:ywqN] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept] [DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.] [NT:similar to hypothetical proteins] [LE:124753] [RE:125298] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503000998_47343_c1_219	2891	6663	132	43		
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000998_5265643_f1_30	2892	6664	1122	373		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000998_5343760_f2_129	2893	6665	267	88		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000998_5860927_f2_138	2894	6666	189	62	75	0.023

Description

gp: [GI:e1283542:g4455153] [LN:ATF6I18] [AC:AL022198] [PN:putative protein]  
 [GN:F6I18.10] [OR:Arabidopsis thaliana] [SR:thale cress] [DB:genpept-pln1]  
 [DE:Arabidopsis thaliana DNA chromosome 4, BAC clone F6I18 (ESSAI project).]  
 [NT:contains EST gb:T22575, T22317] [LE:>199:404:631] [RE:347:548:921]  
 [DI:complementJoin]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000998_6052175_f1_65	2895	6667	153	50		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000998_6053437_c3_310	2896	6668	123	40		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000998_6251262_f3_146	2897	6669	189	62	75	0.0084

Description

gp: [GI:d1044717:g5105618] [LN:AP000062] [AC:AP000062] [PN:121aa long hypothetical protein]  
 [GN:APE1925] [OR:Aeropyrum pernix] [SR:Aeropyrum pernix (strain:K1) DNA]  
 [DB:genpept] [DE:Aeropyrum pernix genomic DNA, section 5/7.] [NT:similar to  
 OWL:AB00947213 percent identity:62.500] [LE:233017] [RE:233382] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000998_657678_f3_208	2898	6670	135	44		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000998_6698526_c2_264	2899	6671	174	57		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000998_6743788_c2_272	2900	6672	132	43		

Description

NO-HIT

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000998_6760887_f3_174	2901	6673	924	307	333	3.8e-30

Description

sp: [LN:GLTC\_BACSU] [AC:P20668] [GN:GLTC] [OR:BACILLUS SUBTILIS] [DE:TRANSCRIPTIONAL REGULATORY PROTEIN GLTC] [SP:P20668] [DB:swissprot] >pir: [LN:A69635] [AC:A69635:A33951:A61642] [PN:transcription activator of glutamate synthase operon gltC:regulatory protein gltC] [GN:gltC] [CL:probable transcription regulator lsyR] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1183504:g2634229] [LN:BSUB0010] [AC:Z99113:AL009126] [PN:transcriptional regulator (LysR family)] [GN:gltC] [FN:positive regulation of the glutamate synthase] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 10 of 21): from 1781201 to 2014980.] [SP:P20668] [LE:232835] [RE:233737] [DI:direct] >gp: [GI:e1185319:g2634240] [LN:BSUB0011] [AC:Z99114:AL009126] [PN:transcriptional regulator (LysR family)] [GN:gltC] [FN:positive regulation of the glutamate synthase] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 11 of 21): from 2000171 to 2207900.] [SP:P20668] [LE:13865] [RE:14767] [DI:direct] >gp: [GI:g457514] [LN:M28509] [AC:M28509] [GN:gltC] [FN:positive transcriptional regulator] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis (gltC) gene, complete cds and glutamate synthase, large subunit (gltA) gene, partial cds. gene.] [LE:34] [RE:936] [DI:complement]

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000998_6832950_c1_218	2902	6674	189	62		

Description

NO-HIT

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000998_956312_f2_139	2903	6675	144	47		

Description

NO-HIT

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000998_984703_c2_281	2904	6676	1026	341	763	1.0e-75

Description

sp: [LN:ABC\_ECOLI] [AC:P30750:P77517] [GN:ABC] [OR:ESCHERICHIA COLI] [DE:ATP-BINDING PROTEIN ABC] [SP:P30750:P77517] [DB:swissprot] >pir: [LN:G64744] [AC:G64744:I41113] [PN:probable ABC-type transport protein abc] [GN:abc] [CL:unassigned ATP-binding cassette proteins: ATP-binding cassette homology] [OR:Escherichia coli] [DB:pir2] >gp: [GI:g1552775] [LN:ECU70214] [AC:U70214] [PN:ATP-binding protein] [GN:abc] [OR:Escherichia coli] [DB:genpept-bct1] [DE:Escherichia coli chromosome minutes 4-6.] [LE:52689] [RE:53720] [DI:complement] >gp: [GI:g1786398] [LN:AE000129] [AC:AE000129:U00096] [PN:ATP-binding component of a transporter] [GN:abc] [FN:transport; Not classified] [OR:Escherichia coli] [DB:genpept-bct2] [DE:Escherichia coli K-12 MG1655 section 19 of 400 of the completest genome.] [NT:f343; 98 pct identical to fragment (231)] [LE:1590] [RE:2621] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_10191427_c1_745	2905	6677	135	44		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_10320337_c3_1119	2906	6678	192	63		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_10359688_f3_663	2907	6679	198	65		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_10546925_c3_1155	2908	6680	978	325	1246	6.8e-127

Description

sp: [LN:DNAA\_STAAU] [AC:P49994] [GN:DNAA] [OR:STAPHYLOCOCCUS AUREUS] [DE:CHROMOSOMAL REPLICATION INITIATOR PROTEIN DNAA] [SP:P49994] [DB:swissprot] >pir: [LN:JC5607] [AC:JC5607] [PN:replication initiation protein dnaA] [GN:dnAA] [CL:replication initiation protein dnaA] [OR:Staphylococcus aureus] [DB:pir2] >gp: [GI:d1014451:g1694677] [LN:D89066] [AC:D89066] [PN:DnaA] [GN:dnAA] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus DNA] [DB:genpept-bct1] [DE:Staphylococcus aureus DNA for DnaA, complete cds.] [LE:456] [RE:1817] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_10556300_f2_428	2909	6681	174	57		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_10556712_c3_1187	2910	6682	990	329	1667	1.7e-171

Description

gp: [GI:g1408063] [LN:STAMECRA] [AC:L14017] [PN:methicillin-resistance protein] [GN:mecR] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus (strain COL) DNA] [DB:genpept-bct1] [DE:Staphylococcus aureus methicillin-resistance protein (mecR) gene and unknown ORF, complete cds.] [NT:putative] [LE:125] [RE:1111] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_10582782_f3_549	2911	6683	141	46		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_10629385_f1_185	2912	6684	153	50		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_10634800_c1_819	2913	6685	966	321	143	2.4e-07

Description

pir: [LN:D69900] [AC:D69900] [PN:conserved hypothetical protein yobV] [GN:yobV] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:g2619048] [LN:AF027868] [AC:AF027868] [PN:transcription regulator] [GN:yobV] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis chromosome region between terC and odhAB.] [NT:similar to Mycobacterium tuberculosis hypothetical] [LE:63061] [RE:64002] [DI:complement] >gp: [GI:e1185382:g2634303] [LN:BSUB0011] [AC:Z99114:AL009126] [GN:yobV] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 11 of 21): from 2000171 to 2207900.] [NT:similar to hypothetical proteins] [LE:82152] [RE:83093] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_1071002_f3_616	2914	6686	411	136	71	0.026

Description

gp: [GI:g142964] [LN:BACGERD] [AC:M27259] [OR:Bacillus subtilis] [SR:B. subtilis (strain 168) DNA, clone lambda-EMBL-3-2H] [DB:genpept-bct1] [DE:B. subtilis gerD gene, complete cds.] [NT:unknown ORF] [LE:<1] [RE:282] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_10727217_f1_212	2915	6687	270	89	212	2.5e-17

Description

pir: [LN:B69770] [AC:B69770] [PN:conserved hypothetical protein ydaS] [GN:ydaS] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:d1020027:g1881247] [LN:AB001488] [AC:AB001488] [GN:ydaS] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:168) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.] [NT:FUNCTION UNKNOWN.] [LE:25711] [RE:25968] [DI:complement] >gp: [GI:e1182403:g2632737] [LN:BSUB0003] [AC:Z99106:AL009126] [GN:ydaS] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 3 of 21): from 402751 to 611850.] [NT:similar to hypothetical proteins from B. subtilis] [LE:89455] [RE:89712] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_10928_c2_1083	2916	6688	1242	413	240	8.2e-18

Description

pir: [LN:T03492] [AC:T03492] [PN:hypothetical protein] [OR:Rhodobacter capsulatus] [DB:pir2] [MP:1] >gp: [GI:g3128293] [LN:AF010496] [AC:AF010496] [PN:hypothetical protein] [OR:Rhodobacter capsulatus] [DB:genpept-bct2] [DE:Rhodobacter capsulatus strain SB1003, partial genome.] [LE:54291] [RE:55613] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_10928_f1_226	2917	6689	1017	338	175	1.3e-10

Description

pir: [LN:T03492] [AC:T03492] [PN:hypothetical protein] [OR:Rhodobacter capsulatus] [DB:pir2] [MP:1] >gp: [GI:g3128293] [LN:AF010496] [AC:AF010496] [PN:hypothetical protein] [OR:Rhodobacter capsulatus] [DB:genpept-bct2] [DE:Rhodobacter capsulatus strain SB1003, partial genome.] [LE:54291] [RE:55613] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_111500_c3_1239	2918	6690	546	181	101	1.9e-05

Description

gp: [GI:g940735] [LN:LMIAP1270] [AC:X85869] [PN:invasive associated protein] [GN:iap] [OR:Listeria monocytogenes] [DB:genpept-bct1] [DE:L.monocytogenes type 1 partial iap gene (strain 12705/89).] [NT:invades nonprofessional phagocytic cells] [LE:<1] [RE:>260] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_111592_c2_931	2919	6691	243	80	83	0.0083

Description

gp: [GI:e1349691:g3880163] [LN:CET24A11] [AC:Z49072] [GN:T24A11.2] [OR:Caenorhabditis elegans] [DB:genpept-inv1] [DE:Caenorhabditis elegans cosmid T24A11, complete sequence.] [LE:22751:23187:23506] [RE:23145:23464:23646] [DI:complementJoin]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_115627_f2_344	2920	6692	168	55		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_1205000_f1_183	2921	6693	555	184	314	4.0e-28

Description

pir: [LN:F69768] [AC:F69768] [PN:acetyltransferase homolog ydaF] [GN:ydaF] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:d1020012:g1881232] [LN:AB001488] [AC:AB001488] [GN:ydaF] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:168) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis genome sequence, 148 kb sequence of the region between 35 and 47 degree.] [NT:PROBABLE ACETYLTRANSFERASE.] [LE:6233] [RE:6784] [DI:direct] >gp: [GI:e1182387:g2632721] [LN:BSUB0003] [AC:Z99106:AL009126] [GN:ydaF] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 3 of 21): from 402751 to 611850.] [NT:similar to acetyltransferase] [LE:69977] [RE:70528] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_12536337_f2_405	2922	6694	327	108		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_12588250_c1_671	2923	6695	198	65		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_1259387_f2_250	2924	6696	126	41		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_1261078_f1_223	2925	6697	579	192	471	9.1e-45

Description

sp: [LN:XPT\_BACSU] [AC:P42085] [GN:XPT] [OR:BACILLUS SUBTILIS] [EC:2.4.2.-] [DE:XANTHINE PHOSPHORIBOSYLTRANSFERASE,] [SP:P42085] [DB:swissprot] >pir:[LN:S51309] [AC:S51309:E69734] [PN:xanthine phosphoribosyltransferase xpt] [GN:xpt] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:g1256617] [LN:BACYACA] [AC:L77246] [PN:adenine phosphoribosyltransferase] [GN:xpt] [FN:purine biosynthesis] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:2.4.2.7] [DE:Bacillus subtilis (YAC10-9 clone) DNA region between the serA and kdg loci.] [NT:27% identity with E.coli adenine] [LE:1426] [RE:2010] [DI:direct] >gp:[GI:e1183653:g2634626] [LN:BSUB0012] [AC:Z99115:AL009126] [PN:xanthine phosphoribosyltransferase] [GN:xpt] [FN:purine biosynthesis] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:2.4.2.7] [DE:Bacillus subtilis complete genome (section 12 of 21): from 2195541 to 2409220.] [SP:P42085] [LE:123142] [RE:123726] [DI:complement] >gp:[GI:g633169] [LN:BSXPTPBUX] [AC:X83878] [PN:xanthine phosphoribosyltransferase] [GN:xpt] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B. subtilis xpt and pbuX genes.] [SP:P42085] [LE:357] [RE:941] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_1301_f3_471	2926	6698	123	40		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_13089052_f1_2	2927	6699	123	40		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_134677_f2_417	2928	6700	1101	366	1373	2.4e-140

Description

sp: [LN:YYAF\_BACSU] [AC:P37518] [GN:YYAF] [OR:BACILLUS SUBTILIS] [DE:REGION] [SP:P37518] [DB:swissprot] >pir:[LN:S66016] [AC:S66016:E70084] [PN:probable GTP-binding protein yyaF] [GN:yyaF] [CL:yeast probable purine nucleotide-binding protein YBR025c] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:d1005764:g467376] [LN:BAC180K] [AC:D26185] [PN:unknown] [OR:Bacillus subtilis] [SR:Bacillus subtilis (sub\_species:Marburg, strain:168) DNA] [DB:genpept-bct1] [DE:B. subtilis DNA, 180 kilobase region of replication origin.] [LE:47839] [RE:48939] [DI:complement] >gp:[GI:e1184818:g2636639] [LN:BSUB0021] [AC:Z99124:AL009126] [GN:yyaF] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 21 of 21): from 3999281 to 4214814.] [NT:similar to hypothetical proteins] [SP:P37518] [LE:199771] [RE:200871] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_13704191_c1_811	2929	6701	171	56		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_13750258_f1_41	2930	6702	162	53		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_1379132_c1_806	2931	6703	564	187	589	2.9e-57

Description

gp: [GI:d1045999:g5360823] [LN:D86934] [AC:D86934] [PN:IS150-like transposase] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus (strain:N315) DNA, clone\_lib:library of N31] [DB:genpept] [DE:Staphylococcus aureus genes, mec region, partial and complete cds.] [NT:ORF N028; putative] [LE:<20180] [RE:20578] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_13828575_f1_31	2932	6704	444	147	617	3.1e-60

Description

sp: [LN:ARSC\_STAAU] [AC:P30330] [GN:ARSC] [OR:STAPHYLOCOCCUS AUREUS] [DE:ARSENATE REDUCTASE (ARSENICAL PUMP MODIFIER)] [SP:P30330] [DB:swissprot] >pir: [LN:D41903] [AC:D41903] [PN:arsenate reductase,] [GN:arsC] [CL:protein-tyrosine-phosphatase, low molecular weight] [OR:Staphylococcus aureus] [EC:1.----] [DB:pir1] >gp: [GI:g150729] [LN:PI2ARSRBC] [AC:M86824] [PN:arsenate reductase] [GN:arsC] [FN:Reduction of arsenate to arsenite] [OR:Plasmid pI258] [SR:Plasmid pI258 DNA] [DB:genpept-bct1] [DE:Plasmid pI258 arsenic resistance operon (arsRBC) genes, completecds.] [LE:1894] [RE:2289] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_1384628_f2_290	2933	6705	1278	425	251	4.3e-19

Description

pir: [LN:H64514] [AC:H64514] [PN:hypothetical protein MJECL41] [OR: Methanococcus jannaschii] [DB:pir2] [MP:ECLREV53908-52610] >gp: [GI:g1522674] [LN:MII2CG] [AC:L77118] [PN:M. jannaschii predicted coding region MJECL41] [GN:MJECL41] [OR: Methanococcus jannaschii] [DB:genpept-bct2] [DE: Methanococcus jannaschii large extra-chromosomal element, completesequence.] [NT:identified by GeneMark; putative] [LE:52610] [RE:53908] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_13864680_c2_1056	2934	6706	384	127	247	5.0e-21

Description

sp: [LN:YQCJ\_BACSU] [AC:P45949] [GN:YQCJ] [OR:BACILLUS SUBTILIS] [DE:HYPOTHETICAL 12.3 KD PROTEIN IN CWLA-CISA INTERGENIC REGION] [SP:P45949] [DB:swissprot] >pir: [LN:H69949] [AC:H69949] [PN:transcription regulator ArsR family homolog yqcJ] [GN:yqcJ] [CL:arsenical resistance operon repressor] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:d1013110:g1303775] [LN:BACJH642] [AC:D84432:D82370] [PN:YqcJ] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:JH642(trpC2 PheA1)) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis DNA, 283 Kb region containing skin element.] [LE:61977] [RE:62294] [DI:direct] >gp: [GI:d1007542:g1217882] [LN:BACSKIN] [AC:D32216] [PN:ORF3] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:JH642 (trpC2 pheA1)) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis 48 kb region including a skin element which islocated between spoIVCB and spoIIIC.] [NT:similarity to arsenical resistance operon] [LE:43732] [RE:44049] [DI:direct] >gp: [GI:e1183810:g2635026] [LN:BSUB0014] [AC:Z99117:AL009126] [GN:yqcJ] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.] [NT:similar to transcriptional regulator (ArsR family)] [SP:P45949] [LE:57136] [RE:57453] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_13912551_c1_827	2935	6707	1695	564	156	6.7e-08

Description

gp: [GI:g4530172] [LN:AF085222] [AC:AF085222] [PN:putative primase] [OR:Streptococcus thermophilus bacteriophage DT1] [DB:genpept-phg] [DE:Streptococcus thermophilus bacteriophage DT1, complete genome.] [NT:Orf36] [LE:28549] [RE:30063] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_14111687_f3_529	2936	6708	225	74	104	3.3e-05

Description

sp: [LN:Y4IQ\_RHISN] [AC:P55500] [GN:Y4IQ, Y4ND, Y4SD] [OR:RHIZOBIUM SP] [SR:NGR234,] [DE:PUTATIVE INSERTION SEQUENCE ATP-BINDING PROTEIN Y4IQ/Y4ND/Y4SD] [SP:P55500] [DB:swissprot] >gp: [GI:g2182455] [LN:AE000079] [AC:AE000079:U00090] [PN:Y4iQ] [GN:y4iQ] [OR:Rhizobium sp. NGR234] [DB:genpept-bct2] [DE:Rhizobium sp. NGR234 plasmid pNGR234a, section 16 of 46 of thecomplete plasmid sequence.] [NT:putative insertion sequence ATP-binding protein;] [LE:1883] [RE:2779] [DI:complement] >gp: [GI:g2182539] [LN:AE000086] [AC:AE000086:U00090] [PN:Y4nD] [GN:y4nD] [OR:Rhizobium sp. NGR234] [DB:genpept-bct2] [DE:Rhizobium sp. NGR234 plasmid pNGR234a, section 23 of 46 of thecomplete plasmid sequence.] [NT:putative insertion sequence ATP-binding protein;] [LE:8640] [RE:9536] [DI:complement] >gp: [GI:g2182618] [LN:AE000095] [AC:AE000095:U00090] [PN:Y4sD] [GN:y4sD] [OR:Rhizobium sp. NGR234] [DB:genpept-bct2] [DE:Rhizobium sp. NGR234 plasmid pNGR234a, section 32 of 46 of thecomplete plasmid sequence.] [NT:putative insertion sequence ATP-binding protein;] [LE:7675] [RE:8571] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_14220027_f3_618	2937	6709	1143	380	190	3.0e-12

Description

gp: [GI:d1025733:g2879913] [LN:D85752] [AC:D85752] [GN:bacG] [OR:Enterococcus faecalis] [SR:Enterococcus faecalis plasmid:pPD1 DNA] [DB:genpept-bct1] [DE:Enterococcus faecalis plasmid pPD1 bacA, bacB, bacC, bacD, bacE,bacF, bacG, bacH and bacI genes, complete cds.] [LE:5832] [RE:7055] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_14460882_c3_1296	2938	6710	342	114	484	3.8e-46

Description

gp: [GI:g1022726] [LN:SHU35635] [AC:U35635] [PN:unknown] [OR:Staphylococcus haemolyticus] [SR:Staphylococcus haemolyticus strain=Y176] [DB:genpept-bct1] [DE:Staphylococcus haemolyticus IS1272 ORF1 and ORF2 genes, completecds.] [NT:ORF1] [LE:1101] [RE:1922] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_14532058_c3_1228	2939	6711	273	90	452	9.4e-43

Description

sp: [LN:TRA1\_STAAU] [AC:P14506] [OR:STAPHYLOCOCCUS AUREUS] [DE:TRANSPOSAE FOR INSERTION SEQUENCE ELEMENT IS257 IN TRANSPOSON TN4003] [SP:P14506] [DB:swissprot]  
>pir: [LN:S04162] [AC:S04162] [PN:transposase 1] [OR:Staphylococcus aureus] [DB:pir2]  
>gp: [GI:g46748] [LN:SATN4003] [AC:X13290] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:Staphylococcus aureus multi-resistance plasmid pSK1 DNA containing transposon Tn4003.] [NT:transposase (AA 1-224)] [SP:P14506] [LE:89] [RE:763] [DI:complement]  
>gp: [GI:g46753] [LN:SATN4003] [AC:X13290] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:Staphylococcus aureus multi-resistance plasmid pSK1 DNA containing transposon Tn4003.] [NT:transposase (AA 1-224)] [SP:P14506] [LE:4017] [RE:4691] [DI:complement]  
>gp: [GI:g1762092] [LN:SEU40381] [AC:U40381] [PN:transposase] [GN:tnp] [OR:Staphylococcus epidermidis] [DB:genpept-bct1] [DE:Staphylococcus epidermidis plasmid pSK697 insertion sequence IS257(697A) putative transposase gene, complete cds.] [NT:Tnp; putative transposase] [LE:57] [RE:731] [DI:direct] >gp: [GI:g1762098] [LN:SEU40384] [AC:U40384] [PN:transposase] [GN:tnp] [OR:Staphylococcus epidermidis] [DB:genpept-bct1] [DE:Staphylococcus epidermidis plasmid pSK818 insertion sequence IS257(818A) putative transposase gene, complete cds.] [NT:Tnp; putative transposase] [LE:57] [RE:731] [DI:direct] >gp: [GI:g3676405] [LN:AF051916] [AC:AF051916] [PN:putative transposase TnpC] [GN:tnpC] [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus plasmid pJE1 remnant of replication proteinRep (rep), trimethoprim resistance protein DfrA (dfrA), thymidylatesynthetase ThyE (thyE), and putative transposase Tnp (tnp) genes, complete cds; and unknown gene.] [LE:65] [RE:739] [DI:direct] >gp: [GI:g3676411] [LN:AF051916] [AC:AF051916] [PN:putative transposase TnpE] [GN:tnpE] [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus plasmid pJE1 remnant of replication proteinRep (rep), trimethoprim resistance protein DfrA (dfrA), thymidylatesynthetase ThyE (thyE), and putative transposase Tnp (tnp) genes, complete cds; and unknown gene.] [LE:4409] [RE:5083] [DI:direct] >gp: [GI:g3676433] [LN:AF051917] [AC:AF051917:L19570] [PN:putative transposase TnpC] [GN:tnpC] [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus plasmid pSK41, complete sequence.] [LE:22981] [RE:23655] [DI:direct] >gp: [GI:g1762090] [LN:SEU40259] [AC:U40259] [PN:Tnp] [GN:tnp] [FN:putative transposase] [OR:Staphylococcus epidermidis] [DB:genpept-bct2] [DE:Staphylococcus epidermidis trimethoprim resistance plasmid pSK639.] [LE:7281] [RE:7955] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_14578382_f1_27	2940	6712	192	63		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_14625031_f3_489	2941	6713	132	43		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_14719827_c3_1275	2942	6714	330	109	85	0.0070

Description

gp: [GI:g4049891] [LN:AF063866] [AC:AF063866] [PN:ORF MSV019 hypothetical protein] [GN:MSV019] [OR:Melanoplus sanguinipes entomopoxvirus] [DB:genpept-vrl] [DE:Melanoplus sanguinipes entomopoxvirus, complete genome.] [LE:21761] [RE:23074] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_14728382_f1_210	2943	6715	300	99	336	1.8e-30

Description

sp: [LN:RS6\_BACSU] [AC:P21468] [GN:RPSF] [OR:BACILLUS SUBTILIS] [DE:30S RIBOSOMAL PROTEIN S6 (BS9)] [SP:P21468] [DB:swissprot] >pir: [LN:S66015] [AC:S66015:S11356:E69699] [PN:ribosomal protein S6 (BS9) rpsF:ribosomal protein BS9] [GN:rpsF] [CL:Escherichia coli ribosomal protein S6] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:d1005763:g467375] [LN:BAC180K] [AC:D26185] [PN:ribosomal protein S6] [GN:rpsF] [OR:Bacillus subtilis] [SR:Bacillus subtilis (sub\_species:Marburg, strain:168) DNA] [DB:genpept-bct1] [DE:B. subtilis DNA, 180 kilobase region of replication origin.] [LE:47441] [RE:47728] [DI:complement] >gp: [GI:e1184817:g2636638] [LN:BSUB0021] [AC:Z99124:AL009126] [PN:ribosomal protein S6 (BS9)] [GN:rpsF] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 21 of 21): from 3999281 to 4214814.] [SP:P21468] [LE:199373] [RE:199660] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_14881552_f1_187	2944	6716	216	71		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_15033181_c3_1093	2945	6717	444	147	90	0.0071

Description

gp: [GI:g4176374] [LN:AC004953] [AC:AC004953] [GN:WUGSC:H\_DJ1059M17.2] [OR:Homo sapiens] [SR:INFORMATION] [DB:genpept-pri3] [DE:Homo sapiens PAC clone DJ1059M17 from 7q21-q31.1, complete sequence.] [NT:myosin regulatory light chain 2; similar to S22715] [LE:67137:67324:69882] [RE:67235:67372:69960] [DI:complementJoin]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_15052318_f2_391	2946	6718	1395	464	1606	4.9e-165

Description

sp: [LN:THDF\_BACSU] [AC:P25811] [GN:THDF] [OR:BACILLUS SUBTILIS] [DE:POSSIBLE THIOPHENE AND FURAN OXIDATION PROTEIN THDF] [SP:P25811] [DB:swissprot] >pir: [LN:JQ1215] [AC:I40439:S66026:C69722:JQ1215:S18075] [PN:thiophen / furan oxidation protein thdF:50K protein homolog] [GN:thdF] [CL:thiophen / furan oxidation protein:translation elongation factor Tu homology] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:d1005774:g467386] [LN:BAC180K] [AC:D26185] [PN:thiophen and furan oxidation] [GN:tdhF] [OR:Bacillus subtilis] [SR:Bacillus subtilis (sub\_species:Marburg, strain:168) DNA] [DB:genpept-bct1] [DE:B. subtilis DNA, 180 kilobase region of replication origin.] [LE:59506] [RE:60885] [DI:complement] >gp: [GI:g40025] [LN:BSORIGS] [AC:X62539] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B. subtilis genes rpmH, rnpA, 50kd, gidA and gidB.] [NT:homologous to E.coli 50K] [SP:P25811] [LE:2515] [RE:3894] [DI:direct] >gp: [GI:e1184828:g2636649] [LN:BSUB0021] [AC:Z99124:AL009126] [GN:thdF] [FN:thiophen and furan oxidation] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 21 of 21): from 3999281 to 4214814.] [SP:P25811] [LE:211438] [RE:212817] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_15055313_c3_1183	2947	6719	444	147	753	1.2e-74

Description

gp: [GI:d1046028:g5360852] [LN:D86934] [AC:D86934] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus (strain:N315) DNA, clone\_lib:library of N31] [DB:genpept] [DE:Staphylococcus aureus genes, mec region, partial and complete cds.] [NT:ORF CN038] [LE:45523] [RE:>45966] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_15632952_c1_833	2948	6720	489	162		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_157500_c1_771	2949	6721	729	242	253	1.2e-21

Description

sp: [LN:YD31\_HELPY] [AC:O25889] [GN:HP1331] [OR:HELICOBACTER PYLORI] [SR:, CAMPYLOBACTER PYLORI] [DE:HYPOTHETICAL PROTEIN HP1331] [SP:O25889] [DB:swissprot] >pir: [LN:C64686] [AC:C64686] [PN:conserved hypothetical integral membrane protein HP1331] [CL:hypothetical protein b2682] [OR:Helicobacter pylori] [DB:pir2] >gp: [GI:g2314496] [LN:AE000634] [AC:AE000634:AE000511] [PN:conserved hypothetical integral membrane] [GN:HP1331] [OR:Helicobacter pylori 26695] [DB:genpept-bct2] [DE:Helicobacter pylori 26695 section 112 of 134 of the complete genome.] [NT:similar to GB:L42023 SP:P44302 PID:1008819] [LE:10600] [RE:11286] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_15752213_f1_167	2950	6722	270	89	74	0.034

Description

gp: [GI:g2645365] [LN:SHU83823] [AC:U83823] [PN:NADH dehydrogenase subunit 4] [GN:ND4] [OR:Mitochondrion Sigmodon hispidus] [SR:Sigmodon hispidus] [DB:genpept-rod] [DE:Sigmodon hispidus NADH dehydrogenase subunit 3 (ND3) and NADHdehydrogenase subunit 4L (ND4L) genes, complete cds, NADHdehydrogenase subunit 4 (ND4) gene, partial cds, and tRNA-Arg gene, complete sequence, mitochondrial genes encoding mitochondrial products.] [LE:709] [RE:>1332] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_15788276_f3_494	2951	6723	198	65	56	0.028

Description

gp: [GI:g452394] [LN:BMFLC3] [AC:Z26886] [PN:Nd-sD mutant fibroin light chain] [OR:Bombyx mori] [SR:domestic silkworm] [DB:genpept-inv1] [DE:B.mori gene for Nd-sD mutant fibroin light chain.] [LE:<1:1275:1732] [RE:125:1447:2074] [DI:directJoin]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_15893843_f2_246	2952	6724	135	44		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_161661_f3_507	2953	6725	147	48		

Description

NO-HIT

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_16222092_f1_44	2954	6726	141	46		

Description

NO-HIT

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_162812_c2_1058	2955	6727	147	48		

Description

NO-HIT

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_16432963_c1_709	2956	6728	1116	371	972	7.4e-98

Description

pir: [LN:A69847] [AC:A69847] [PN:cystathione gamma-synthase homolog yjcI] [GN:yjcI] [CL:O-succinylhomoserine (thiol)-lyase] [OR:Bacillus subtilis] [DB:pir2]  
 >gp: [GI:e1183207:g2633541] [LN:BSUB0007] [AC:Z99110:AL009126] [GN:yjcI] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 7 of 21): from 1194391 to 1411140.] [NT:similar to cystathione gamma-synthase] [LE:63573] [RE:64694] [DI:direct]

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_16601512_c1_834	2957	6729	510	169	98	0.0027

Description

gp: [GI:e1346924:g3877219] [LN:CEF46F3] [AC:Z81085] [GN:F46F3.3] [OR:Caenorhabditis elegans] [DB:genpept-inv1] [DE:Caenorhabditis elegans cosmid F46F3, complete sequence.] [LE:12629:13473:14592:14734] [RE:12740:13771:14687:14877] [DI:directJoin]

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_16688_c2_1062	2958	6730	216	71	95	6.4e-05

Description

gp: [GI:g5230679] [LN:AF036485] [AC:AF036485:AF036486:AF036487:U93364] [PN:hypothetical protein] [OR:Plasmid pNZ4000] [DB:genpept] [DE:Plasmid pNZ4000, complete sequence.] [NT:Orf-100] [LE:42675:1] [RE:42810:167] [DI:complementJoin]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_16695311_f2_259	2959	6731	693	230	1184	2.5e-120

Description

sp: [LN:TRA2\_STAAU] [AC:P19380] [OR:STAPHYLOCOCCUS AUREUS] [DE:TRANSPOASE FOR INSERTION SEQUENCE-LIKE ELEMENT IS431MEC] [SP:P19380] [DB:swissprot] >pir: [LN:S12093] [AC:S12093:JU0116] [PN:probable transposase] [OR:Staphylococcus aureus] [DB:pir2] >gp: [GI:g46602] [LN:SAIS431M] [AC:X53818:M18438] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:S. aureus IS431mec gene associated with methicillin resistance.] [NT:putative transposase (AA 1 - 224)] [SP:P19380] [LE:272] [RE:946] [DI:direct] >gp: [GI:e1237900:g2791991] [LN:SAMECAR1I] [AC:Y14051] [PN:putative transposase] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:Staphylococcus aureus mecA, mecR1, mecI genes and ORF168, ORF142, ORF44, ORF145 and ORF224.] [NT:ORF224] [LE:8096] [RE:8770] [DI:direct] >gp: [GI:d1046034:g5360858] [LN:D86934] [AC:D86934] [PN:transposase for insertion sequence-like element] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus (strain:N315) DNA, clone\_lib:library of N31] [DB:genpept] [DE:Staphylococcus aureus genes, mec region, partial and complete cds.] [NT:ORF N062] [LE:48054] [RE:48728] [DI:direct] >gp: [GI:d1046044:g5360868] [LN:D86934] [AC:D86934] [PN:transposase for insertion sequence-like element] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus (strain:N315) DNA, clone\_lib:library of N31] [DB:genpept] [DE:Staphylococcus aureus genes, mec region, partial and complete cds.] [NT:ORF N070] [LE:53400] [RE:54074] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_16695311_f2_282	2960	6732	693	230	1191	4.6e-121

Description

sp: [LN:TRA2\_STAAU] [AC:P19380] [OR:STAPHYLOCOCCUS AUREUS] [DE:TRANSPOASE FOR INSERTION SEQUENCE-LIKE ELEMENT IS431MEC] [SP:P19380] [DB:swissprot] >pir: [LN:S12093] [AC:S12093:JU0116] [PN:probable transposase] [OR:Staphylococcus aureus] [DB:pir2] >gp: [GI:g46602] [LN:SAIS431M] [AC:X53818:M18438] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:S. aureus IS431mec gene associated with methicillin resistance.] [NT:putative transposase (AA 1 - 224)] [SP:P19380] [LE:272] [RE:946] [DI:direct] >gp: [GI:e1237900:g2791991] [LN:SAMECAR1I] [AC:Y14051] [PN:putative transposase] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:Staphylococcus aureus mecA, mecR1, mecI genes and ORF168, ORF142, ORF44, ORF145 and ORF224.] [NT:ORF224] [LE:8096] [RE:8770] [DI:direct] >gp: [GI:d1046034:g5360858] [LN:D86934] [AC:D86934] [PN:transposase for insertion sequence-like element] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus (strain:N315) DNA, clone\_lib:library of N31] [DB:genpept] [DE:Staphylococcus aureus genes, mec region, partial and complete cds.] [NT:ORF N062] [LE:48054] [RE:48728] [DI:direct] >gp: [GI:d1046044:g5360868] [LN:D86934] [AC:D86934] [PN:transposase for insertion sequence-like element] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus (strain:N315) DNA, clone\_lib:library of N31] [DB:genpept] [DE:Staphylococcus aureus genes, mec region, partial and complete cds.] [NT:ORF N070] [LE:53400] [RE:54074] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_16975082_c1_860	2961	6733	306	101		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_17004551_f1_11	2962	6734	144	47		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503000999_193812_c1_810	2963	6735	129	42		
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503000999_19531308_c1_778	2964	6736	129	42		
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503000999_19548192_c3_1120	2965	6737	765	254	68	0.00074
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Description

pir:[LN:S44477] [AC:S44477:S58747] [PN:NADH dehydrogenase (ubiquinone), chain 4L] [GN:ND4L] [CL:NADH dehydrogenase (ubiquinone) chain 4L] [OR:mitochondrion Hansenula wingei] [EC:1.6.5.3] [DB:pir2]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503000999_1960300_f1_181	2966	6738	201	66		
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503000999_19613436_f2_338	2967	6739	162	53		
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503000999_19647213_c3_1213	2968	6740	342	113	157	1.7e-11
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Description

pir:[LN:C69774] [AC:C69774] [PN:transcription regulator phage-related homolog ydcN] [GN:ydcN] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:d1020073:g1881293] [LN:AB001488] [AC:AB001488] [GN:ydcN] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:168) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.] [NT:PROBABLE REPRESSOR PROTEIN.] [LE:64366] [RE:64749] [DI:complement] >gp:[GI:e1182448:g2632782] [LN:BSUB0003] [AC:Z99106:AL009126] [GN:ydcN] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.] [NT:similar to transcriptional regulator] [LE:128111] [RE:128494] [DI:complement]

ORF Name	NTID	AAID	NT Length	AA Length	score	probability
AI7503000999_19719812_c1_877	2969	6741	474	157	803	6.0e-80

#### Description

sp: [LN:TRA1\_STAAU] [AC:P14506] [OR:STAPHYLOCOCCUS AUREUS] [DE:TRANSPOSAE FOR INSERTION SEQUENCE ELEMENT IS257 IN TRANSPOSON TN4003] [SP:P14506] [DB:swissprot]  
>pir: [LN:S04162] [AC:S04162] [PN:transposase 1] [OR:Staphylococcus aureus] [DB:pir2]  
>gp: [GI:g46748] [LN:SATN4003] [AC:X13290] [OR:Staphylococcus aureus] [DB:genpept-bct1]  
[DE:Staphylococcus aureus multi-resistance plasmid pSK1 DNA containingtransposon  
Tn4003.] [NT:transposase (AA 1-224)] [SP:P14506] [LE:89] [RE:763] [DI:complement]  
>gp: [GI:g46753] [LN:SATN4003] [AC:X13290] [OR:Staphylococcus aureus] [DB:genpept-bct1]  
[DE:Staphylococcus aureus multi-resistance plasmid pSK1 DNA containingtransposon  
Tn4003.] [NT:transposase (AA 1-224)] [SP:P14506] [LE:4017] [RE:4691] [DI:complement]  
>gp: [GI:g1762092] [LN:SEU40381] [AC:U40381] [PN:transposase] [GN:tnp]  
[OR:Staphylococcus epidermidis] [DB:genpept-bct1] [DE:Staphylococcus epidermidis plasmid  
pSK697 insertion sequenceIS257(697A) putative transposase gene, complete cds.] [NT:Tnp;  
putative transposase] [LE:57] [RE:731] [DI:direct] >gp: [GI:g1762098] [LN:SEU40384]  
[AC:U40384] [PN:transposase] [GN:tnp] [OR:Staphylococcus epidermidis] [DB:genpept-bct1]  
[DE:Staphylococcus epidermidis plasmid pSK818 insertion sequenceIS257(818A) putative  
transposase gene, complete cds.] [NT:Tnp; putative transposase] [LE:57] [RE:731]  
[DI:direct] >gp: [GI:g3676405] [LN:AF051916] [AC:AF051916] [PN:putative transposase  
TnpC] [GN:tnpC] [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus  
plasmid pJE1 remnant of replication proteinRep (rep), trimethoprim resistance protein  
DfrA (dfrA), thymidylatesynthetase ThyE (thyE), and putative transposase Tnp (tnp)  
genes, complete cds; and unknown gene.] [LE:65] [RE:739] [DI:direct] >gp: [GI:g3676411]  
[LN:AF051916] [AC:AF051916] [PN:putative transposase TnpE] [GN:tnpE] [OR:Staphylococcus  
aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus plasmid pJE1 remnant of replication  
proteinRep (rep), trimethoprim resistance protein DfrA (dfrA), thymidylatesynthetase  
ThyE (thyE), and putative transposase Tnp (tnp) genes, complete cds; and unknown gene.]  
[LE:4409] [RE:5083] [DI:direct] >gp: [GI:g3676433] [LN:AF051917] [AC:AF051917:L19570]  
[PN:putative transposase TnpC] [GN:tnpC] [OR:Staphylococcus aureus] [DB:genpept-bct2]  
[DE:Staphylococcus aureus plasmid pSK41, complete sequence.] [LE:22981] [RE:23655]  
[DI:direct] >gp: [GI:g1762090] [LN:SEU40259] [AC:U40259] [PN:Tnp] [GN:tnp] [FN:putative  
transposase] [OR:Staphylococcus epidermidis] [DB:genpept-bct2] [DE:Staphylococcus  
epidermidis trimethoprim resistance plasmid pSK639.] [LE:7281] [RE:7955] [DI:direct]

ORF Name	NTID	AAID	NT Length	AA Length	score	probability
AI7503000999_19720462_f2_314	2970	6742	1203	400	370	4.6e-34

#### Description

sp: [LN:YJIJ\_ECOLI] [AC:P39381] [GN:YJIJ] [OR:ESCHERICHIA COLI] [DE:HYPOTHETICAL 41.4 KD  
PROTEIN IN IADA-MCRD INTERGENIC REGION (F392)] [SP:P39381] [DB:swissprot]  
>pir: [LN:S56557] [AC:S56557:F65247] [PN:hypothetical 41.4K protein (iadA-mcrD  
intergenic region):hypothetical protein f392] [GN:yjiJ] [OR:Escherichia coli]  
[DB:pir2] >gp: [GI:g537173] [LN:ECOUW93] [AC:U14003] [OR:Escherichia coli]  
[DB:genpept-bct1] [DE:Escherichia coli K-12 chromosomal region from 92.8 to 00.1  
minutes.] [NT:ORF\_f392] [LE:252329] [RE:253507] [DI:complement] >gp: [GI:g1790788]  
[LN:AE000503] [AC:AE000503:U00096] [PN:putative transport protein] [GN:yjiJ]  
[FN:putative transport; Not classified] [OR:Escherichia coli] [DB:genpept-bct2]  
[DE:Escherichia coli K-12 MG1655 section 393 of 400 of the complete genome.] [NT:f392;  
100 pct identical amino acid sequence and] [LE:10037] [RE:11215] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_19767150_c3_1177	2971	6743	567	188	746	6.6e-74

Description

gp: [GI:d1046049:g5360873] [LN:D86934] [AC:D86934] [PN:orfX] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus (strain:N315) DNA, clone\_lib:library of N31] [DB:genpept] [DE:Staphylococcus aureus genes, mec region, partial and complete cds.] [NT:ORF CN051] [LE:56338] [RE:>56817] [DI:complement] >gp: [GI:d1046058:g5391439] [LN:AB014440] [AC:AB014440] [PN:orfX] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus (strain:NCTC8325) DNA] [DB:genpept] [DE:Staphylococcus aureus genes for orf1, orfX, orf2, orf3, partial and complete cds.] [NT:integration site of mecDNA was predicted to locate] [LE:1396] [RE:1875] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_19803150_f2_421	2972	6744	129	42		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_20194532_c1_732	2973	6745	156	51		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_20329376_f1_94	2974	6746	174	57	57	0.013

Description

pir: [LN:D70158] [AC:D70158] [PN:lipoprotein signal peptidase,] [OR: *Borrelia burgdorferi*] [SR:, Lyme disease spirochete] [EC:3.4.23.36] [DB:pir2] >gp: [GI:g2688373] [LN:AE001151] [AC:AE001151:AE000783] [PN:signal peptidase II (lsp)] [GN:BB0469] [OR: *Borrelia burgdorferi*] [SR:Lyme disease spirochete] [DB:genpept-bct2] [DE: *Borrelia burgdorferi* (section 37 of 70) of the complete genome.] [NT:similar to GB:X78084 PID:459545 SP:Q59835 percent] [LE:10907] [RE:11419] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_20359682_f1_169	2975	6747	168	55		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_20517318_f1_193	2976	6748	1200	399	1171	6.1e-119

Description

gp: [GI:e281310:g1667356] [LN:CTZ82038] [AC:Z82038] [PN:acetyl coenzyme A acetyltransferase (thiolase)] [GN:thlA] [OR: *Thermoanaerobacterium thermosaccharolyticum*] [DB:genpept-bct1] [EC:2.3.1.9] [DE: *C. thermosaccharolyticum* etfB, etfA, hbd, thlA and actA genes.] [LE:2642] [RE:3820] [DI:direct] >gp: [GI:e308220:g1903332] [LN:TTBCSOPRN] [AC:Z92974] [PN:acetyl coenzyme A acetyltransferase (thiolase)] [GN:thl] [OR: *Thermoanaerobacterium thermosaccharolyticum*] [DB:genpept-bct1] [EC:2.3.1.9] [DE: *T. thermosaccharolyticum* BCS operon DNA.] [LE:4835] [RE:6013] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_20523253_c3_1227	2977	6749	252	83	447	3.2e-42

Description

sp: [LN:TRA1\_STAAU] [AC:P14506] [OR:STAPHYLOCOCCUS AUREUS] [DE:TRANSPOSAE FOR INSERTION SEQUENCE ELEMENT IS257 IN TRANSPOSON TN4003] [SP:P14506] [DB:swissprot]  
>pir: [LN:S04162] [AC:S04162] [PN:transposase 1] [OR:Staphylococcus aureus] [DB:pir2]  
>gp: [GI:g46748] [LN:SATN4003] [AC:X13290] [OR:Staphylococcus aureus] [DB:genpept-bct1]  
[DE:Staphylococcus aureus multi-resistance plasmid pSK1 DNA containing transposon  
Tn4003.] [NT:transposase (AA 1-224)] [SP:P14506] [LE:89] [RE:763] [DI:complement]  
>gp: [GI:g46753] [LN:SATN4003] [AC:X13290] [OR:Staphylococcus aureus] [DB:genpept-bct1]  
[DE:Staphylococcus aureus multi-resistance plasmid pSK1 DNA containing transposon  
Tn4003.] [NT:transposase (AA 1-224)] [SP:P14506] [LE:4017] [RE:4691] [DI:complement]  
>gp: [GI:g1762092] [LN:SEU40381] [AC:U40381] [PN:transposase] [GN:tnp]  
[OR:Staphylococcus epidermidis] [DB:genpept-bct1] [DE:Staphylococcus epidermidis plasmid  
pSK697 insertion sequence IS257(697A) putative transposase gene, complete cds.] [NT:Tnp;  
putative transposase] [LE:57] [RE:731] [DI:direct] >gp: [GI:g1762098] [LN:SEU40384]  
[AC:U40384] [PN:transposase] [GN:tnp] [OR:Staphylococcus epidermidis] [DB:genpept-bct1]  
[DE:Staphylococcus epidermidis plasmid pSK818 insertion sequence IS257(818A) putative  
transposase gene, complete cds.] [NT:Tnp; putative transposase] [LE:57] [RE:731]  
[DI:direct] >gp: [GI:g3676405] [LN:AF051916] [AC:AF051916] [PN:putative transposase  
TnpC] [GN:tnpC] [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus  
plasmid pJE1 remnant of replication protein Rep (rep), trimethoprim resistance protein  
DfrA (dfrA), thymidylatesynthetase ThyE (thyE), and putative transposase Tnp (tnp)  
genes, complete cds; and unknown gene.] [LE:65] [RE:739] [DI:direct] >gp: [GI:g3676411]  
[LN:AF051916] [AC:AF051916] [PN:putative transposase TnpE] [GN:tnpE] [OR:Staphylococcus  
aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus plasmid pJE1 remnant of replication  
protein Rep (rep), trimethoprim resistance protein DfrA (dfrA), thymidylatesynthetase  
ThyE (thyE), and putative transposase Tnp (tnp) genes, complete cds; and unknown gene.]  
[LE:4409] [RE:5083] [DI:direct] >gp: [GI:g3676433] [LN:AF051917] [AC:AF051917:L19570]  
[PN:putative transposase TnpC] [GN:tnpC] [OR:Staphylococcus aureus] [DB:genpept-bct2]  
[DE:Staphylococcus aureus plasmid pSK41, complete sequence.] [LE:22981] [RE:23655]  
[DI:direct] >gp: [GI:g1762090] [LN:SEU40259] [AC:U40259] [PN:Tnp] [GN:tnp] [FN:putative  
transposase] [OR:Staphylococcus epidermidis] [DB:genpept-bct2] [DE:Staphylococcus  
epidermidis trimethoprim resistance plasmid pSK639.] [LE:7281] [RE:7955] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_20585963_c3_1206	2978	6750	348	115	478	1.7e-45

Description

gp: [GI:d1045998:g5360822] [LN:D86934] [AC:D86934] [PN:IS150-like transposase]  
[OR:Staphylococcus aureus] [SR:Staphylococcus aureus (strain:N315) DNA,  
clone\_lib:library of N31] [DB:genpept] [DE:Staphylococcus aureus genes, mec region,  
partial and complete cds.] [NT:ORF N027; putative] [LE:19826] [RE:20179] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_20585963_c3_1283	2979	6751	906	301	647	2.0e-63

Description

gp: [GI:g929972] [LN:BAU30714] [AC:U30714] [OR:Bacillus anthracis] [SR:plasmid pXO1] [DB:genpept-bct1] [DE:Bacillus anthracis Weybridge A toxin plasmid pXO1 right invertedrepeat element (WeyAR) bordering the toxin-encoding region, ORFAand ORFB genes, complete cds.] [NT:ORFB; similar to B. anthracis SterneL element ORFB;] [LE:512] [RE:1336] [DI:direct] >gp: [GI:g929975] [LN:BAU30715] [AC:U30715] [OR:Bacillus anthracis] [SR:plasmid pXO1] [DB:genpept-bct1] [DE:Bacillus anthracis Sterne toxin plasmid pXO1 left inverted repeatelement (SterneL) bordering the toxin-encoding region, ORFB andtruncated ORFA genes, complete cds.] [NT:ORFB; similar to B. anthracis WeyAR element ORFB;] [LE:458] [RE:1282] [DI:direct] >gp: [GI:g4894312] [LN:AF065404] [AC:AF065404] [PN:pXO1-96] [OR:Bacillus anthracis] [DB:genpept-bct2] [DE:Bacillus anthracis virulence plasmid PX01, complete sequence.] [LE:116307] [RE:117131] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_20964212_c3_1232	2980	6752	1692	563	652	6.0e-64

Description

gp: [GI:d1046002:g5360826] [LN:D86934] [AC:D86934] [PN:site-specific recombinase] [GN:ccrB] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus (strain:N315) DNA, clone\_lib:library of N31] [DB:genpept] [DE:Staphylococcus aureus genes, mec region, partial and complete cds.] [NT:ORF N037; cassette chromosome recombinase B] [LE:25508] [RE:27136] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_2116643_f3_472	2981	6753	189	62	47	0.0062

Description

sp: [LN:TYB4\_MOUSE] [AC:P20065] [GN:TMSB4:PTMB4] [OR:MUS MUSCULUS] [SR:, MOUSE] [DE:THYMOSIN BETA-4] [SP:P20065] [DB:swissprot] >pir: [LN:A37217] [AC:A37217:S08074:S12884] [PN:thymosin beta-4] [CL:thymosin beta] [OR:Mus musculus] [SR:, house mouse] [DB:pir2] >gp: [GI:g54794] [LN:MMTHYB4] [AC:X16053:M38039:M54991] [OR:Mus musculus] [SR:house mouse] [DB:genpept-rod] [DE:Mouse mRNA for thymosin beta-4.] [NT:thymosin beta-4a (AA 1 - 50)] [SP:P20065] [LE:140] [RE:292] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_2120265_c3_1214	2982	6754	870	289	151	6.1e-08

Description

pir: [LN:S76167] [AC:S76167] [PN:hypothetical protein] [OR:Synechocystis sp.] [SR:PCC 6803, , PCC 6803] [SR:PCC 6803, ] [DB:pir2] >gp: [GI:d1019159:g1653513] [LN:D90914] [AC:D90914:AB001339] [PN:hypothetical protein] [OR:Synechocystis sp.] [SR:Synechocystis sp. (strain:PCC6803) DNA] [DB:genpept-bct1] [DE:Synechocystis sp. PCC6803 complete genome, 16/27, 1991550-2137258.] [NT:ORF\_ID:slr0959] [LE:37283] [RE:38872] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_2128400_f1_188	2983	6755	138	45		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_2148468_f2_400	2984	6756	2073	690	1718	6.6e-177

Description

gp: [GI:g3789932] [LN:AF090142] [AC:AF090142] [PN:lipase precursor] [GN:gehD] [OR:Staphylococcus epidermidis] [DB:genpept-bct2] [EC:3.1.1.3] [DE:Staphylococcus epidermidis lipase precursor (gehD) gene, completecds.] [NT:GehD] [LE:293] [RE:2224] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_21506575_c1_702	2985	6757	897	298	331	6.2e-30

Description

pir: [LN:JC5911] [AC:JC5911] [PN:lysin] [GN:lys] [OR:Lactobacillus phage phi-gle] [DB:pir2]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_21521878_c1_795	2986	6758	354	117	181	1.2e-12

Description

pir: [LN:F64114] [AC:F64114] [PN:type I site-specific deoxyribonuclease, chain hsdR] [GN:hsdR] [CL:DEAD/H box helicase homology] [OR:Haemophilus influenzae] [EC:3.1.21.3] [DB:pir2] >gp: [GI:g1574743] [LN:U32808] [AC:U32808:L42023] [PN:type I restriction enzyme (hsdR)] [GN:HI1285] [OR:Haemophilus influenzae Rd] [DB:genpept-bct2] [DE:Haemophilus influenzae Rd section 123 of 163 of the completegenome.] [NT:similar to PID:1685100 percent identity: 59.01;] [LE:5702] [RE:8869] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_21532937_f2_349	2987	6759	129	42		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_21644175_c3_1179	2988	6760	273	90	439	2.2e-41

Description

gp: [GI:d1046045:g5360869] [LN:D86934] [AC:D86934] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus (strain:N315) DNA, clone\_lib:library of N31] [DB:genpept] [DE:Staphylococcus aureus genes, mec region, partial and complete cds.] [NT:ORF CN049] [LE:54106] [RE:>54378] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_21660805_f1_145	2989	6761	1017	338	867	9.9e-87

Description

gp: [GI:g3044072] [LN:AF055713] [AC:AF055713] [PN:beta-hemolysin] [GN:hlp] [OR:Staphylococcus schleiferi] [DB:genpept-bct2] [DE:Staphylococcus schleiferi beta-hemolysin (hlp) gene, partial cds.] [LE:1] [RE:>987] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_21736277_f2_365	2990	6762	171	56		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_22078331_f2_355	2991	6763	180	59		

Description

NO-HIT

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_2209675_f1_61	2992	6764	1470	489	465	3.9e-44

Description

sp: [LN:TYD2\_PETCR] [AC:Q06086] [GN:TYRDC-2] [OR:PETROSELINUM CRISPUM]  
 [SR:, PARSLEY:PETROSELINUM HORTENSE] [EC:4.1.1.25] [DE:TYROSINE DECARBOXYLASE 2,]  
 [SP:Q06086] [DB:swissprot] >pir: [LN:A44405] [AC:A44405] [PN:tyrosine decarboxylase,]  
 [GN:tyrCD] [CL:aromatic-L-amino-acid decarboxylase:animal histidine decarboxylase  
 homology] [OR:Petroselinum crispum] [SR:, parsley] [EC:4.1.1.25] [DB:pir2]  
 >gp: [GI:g169671] [LN:PUMTRYDC2X] [AC:M96070] [PN:tyrosine decarboxylase] [GN:TryDC-2]  
 [OR:Petroselinum crispum] [SR:Petroselinum crispum (library: lambda gt11) cDNA to mRNA]  
 [DB:genpept-pln1] [EC:4.1.1.25] [DE:Parsley tyrosine decarboxylase (TryDC-2) mRNA,  
 complete cds.] [LE:4] [RE:1548] [DI:direct]

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_2214217_c2_984	2993	6765	1845	614	2888	6.9e-301

Description

gp: [GI:g5114231] [LN:AF136709] [AC:AF136709] [PN:histidine kinase YycG] [GN:yyCG]  
 [OR:Staphylococcus aureus] [DB:genpept] [DE:Staphylococcus aureus response regulator  
 YycF (yyCF) and histidine kinase YycG (yyCG) genes, complete cds.] [LE:1363] [RE:3189]  
 [DI:direct]

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_22275082_f2_264	2994	6766	135	44		

Description

NO-HIT

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_22291327_c2_908	2995	6767	141	46		

Description

NO-HIT

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_22383437_f2_293	2996	6768	321	106	80	0.0091

Description

pir: [LN:S29577] [AC:I51043:S29577] [PN:Ig light chain] [GN:IgL] [OR:Oncorhynchus  
 mykiss] [SR:, rainbow trout] [DB:pir2]

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_22475037_c3_1209	2997	6769	126	41	114	2.3e-06

Description

gp: [GI:g2605928] [LN:AF029727] [AC:AF029727] [OR:Enterococcus faecium]  
 [DB:genpept-bct2] [DE:Enterococcus faecium insertion sequence IS1485, complete  
 sequence.] [NT:putative; orfB] [LE:402] [RE:1238] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_22537563_c1_840	2998	6770	231	76		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_22679825_f1_84	2999	6771	168	55	111	7.6e-06

Description

pir: [LN:B69978] [AC:B69978] [PN:2-nitropropane dioxygenase homolog yrpB] [GN:ypdB] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:g1934639] [LN:BSU93875] [AC:U93875] [PN:2-nitropropane dioxygenase] [GN:ypdB] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis alcohol dehydrogenase (adhB) gene, partial cds, hypothetical spore coat protein (yraF), hypothetical spore coatprotein (yraG), YraH (yraH), YraI (yraI), YraJ (yraJ), YraK (yraK), YraL (yraL), chitosanase precursor (csn), YraM (yraM), LysR-familytranscription regulator (yraN), YraO (yraO), YrpG (ypG), RNAPolymerase sigma factor SigZ (sigZ), YrpE (ypE), YrpD (ypD), YrpC(ypC) and 2-nitropropane dioxygenase (ypB) genes, complete cds, and aminoglycoside 6-adenylyltransferase (aadK) gene, partial cds.] [NT:similar to 2-nitropropane dioxygenase of Williopsis] [LE:16473] [RE:17516] [DI:complement] >gp: [GI:e1183909:g2635125] [LN:BSUB0014] [AC:Z99117:AL009126] [GN:ypdB] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.] [NT:similar to 2-nitropropane dioxygenase] [LE:136734] [RE:137777] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_22900337_c2_906	3000	6772	135	44		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_22902302_c1_767	3001	6773	1407	468	2010	7.5e-208

Description

sp: [LN:SYS\_STAAU] [AC:P95689] [GN:SERS] [OR:STAPHYLOCOCCUS AUREUS] [EC:6.1.1.11] [DE:SERYL-TRNA SYNTHETASE, (SERINE--TRNA LIGASE) (SERRS)] [SP:P95689] [DB:swissprot] >gp: [GI:e291101:g1835218] [LN:SASERS] [AC:Y09924] [PN:seryl-trna synthetase] [GN:serS] [OR:Staphylococcus aureus] [DB:genpept-bct1] [EC:6.1.1.11] [DE:S.aureus serS gene.] [SP:P95689] [LE:1] [RE:1287] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_23437803_f3_452	3002	6774	714	237	129	7.7e-07

Description

gp: [GI:g4981720] [LN:AE001774] [AC:AE001774:AE000512] [PN:transcriptional regulator, crp family] [GN:TM1171] [OR:Thermotoga maritima] [DB:genpept-bct2] [DE:Thermotoga maritima section 86 of 136 of the complete genome.] [NT:similar to GB:Z26044 SP:P47200 PID:398391 percent] [LE:5164] [RE:5769] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_23438301_f1_87	3003	6775	255	84		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_23438876_f3_528	3004	6776	258	85		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_23439193_c3_1263	3005	6777	495	164	453	7.4e-43

Description

pir: [LN:G69784] [AC:G69784] [PN:hypothetical protein ydhK] [GN: ydhK] [OR: Bacillus subtilis] [DB:pir2] >gp: [GI:e1182558:g2632892] [LN:BSUB0004] [AC:Z99107:AL009126] [GN: ydhK] [FN:unknown] [OR: Bacillus subtilis] [DB:genpept-bct1] [DE: Bacillus subtilis complete genome (section 4 of 21): from 600701 to 813890.] [LE:23509] [RE:24126] [DI:direct] >gp: [GI:d1020482:g1945095] [LN:D88802] [AC:D88802] [GN: ydhK] [OR: Bacillus subtilis] [SR: Bacillus subtilis (sub\_species:Marburg, strain:168, isolate:JH642] [DB:genpept-bct1] [DE: Bacillus subtilis DNA for phoB-rrnE-groESL region, complete cds.] [NT:membrane protein] [LE:10511] [RE:11128] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_2345025_c2_913	3006	6778	144	47		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_23462762_c3_1097	3007	6779	1527	508	2298	2.3e-238

Description

sp: [LN:AHPF\_STAAU] [AC:O05204] [GN:AHPF] [OR:STAPHYLOCOCCUS AUREUS] [EC:1.6.4.-] [DE:ALKYL HYDROPEROXIDE REDUCTASE SUBUNIT F,] [SP:O05204] [DB:swissprot] >gp: [GI:g1916317] [LN:SAU92441] [AC:U92441:X85029] [PN:alkyl hydroperoxide reductase subunit F] [GN:ahpF] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:Staphylococcus aureus alkyl hydroperoxide reductase subunit C(aphC) and subunit F (aphF) genes, complete cds.] [NT:AhpF] [LE:1376] [RE:2899] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_23468762_f3_521	3008	6780	132	43		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_23507_c1_765	3009	6781	2709	902	3998	0.0

Description

gp: [GI:d1001842:g540542] [LN:STAGYRABA] [AC:D10489] [PN:DNA gyrase A] [GN:gyrA] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus (strain:ATCC12600) DNA] [DB:genpept-bct1] [EC:5.99.1.3] [DE:Staphylococcus aureus genes for DNA gyrase A and B, complete cds.] [LE:2152] [RE:4815] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_23537785_f2_233	3010	6782	138	45		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_23538427_c2_887	3011	6783	309	102	132	8.3e-09

Description

pir: [LN:F71456] [AC:F71456] [PN:hypothetical protein PH0308] [GN:PH0308] [OR:Pyrococcus horikoshii] [DB:pir2] >gp: [GI:d1030324:g3256698] [LN:AP000001] [AC:AP000001:AB009465:AB009464:AB009466:AB009467:AB009468:AB009469] [PN:215aa long hypothetical protein] [GN:PH0308] [OR:Pyrococcus horikoshii] [SR:Pyrococcus horikoshii (strain:OT3) DNA] [DB:genpept-bct1] [DE:Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt. position (1/7).] [NT:motif=prokaryotic membrane lipoprotein lipid] [LE:271764] [RE:272411] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_23556577_f1_99	3012	6784	324	107		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_23563500_c1_706	3013	6785	156	51		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_235678_f2_239	3014	6786	216	71	203	2.3e-16

Description

pir: [LN:F69903] [AC:F69903] [PN:D-alanyl-D-alanine carboxypeptidase homolog yodJ] [GN:yodJ] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:g2415396] [LN:AF015775] [AC:AF015775] [PN:carboxypeptidase] [GN:yodJ] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis YodA (yodA), YodB (yodB), YodC (yodC), YodD (yodD), ABC-transporter (yodE), permease (yodF), proteinase (ctpA), YodH (yodH), YodI (yodI), carboxypeptidase (yodJ), purinenucleoside phosphorylase (deoD), YodL (yodL), YodM (yodM), YodN (yodN), YodO (yodO), YodP (yodP), acetylornithine deacetylase (argE), butyrate-acetoacetate CoA transferase (yodR), butyrateacetoacetate-CoA transferase (yodS), YodT (yodT), CgeE (cgeE), CgeD (cgeD), CgeC (cgeC), CgeA (cgeA), CgeB (cgeB), YzxA (yzxA), UDP-glucose epimerase (yodU), YodV (yodV), and YodW (yodW) genes, complete cds; and YodZ (yodZ) gene, partial cds.] [NT:similar to Enterococcus faecium D-alanyl-D-alanine] [LE:8510] [RE:9331] [DI:complement] >gp: [GI:e1185433:g2634354] [LN:BSUB0011] [AC:Z99114:AL009126] [GN:yodJ] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.] [NT:similar to D-alanyl-D-alanine carboxypeptidase] [LE:133640] [RE:134461] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_23610885_c1_820	3015	6787	126	41		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000999_23610952_c2_1082	3016	6788	855	284	305	3.6e-27
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Description

pir: [LN:H69468] [AC:H69468] [PN:lysophospholipase homolog] [OR:Archaeoglobus fulgidus] [DB:pir2] >gp: [GI:g2648798] [LN:AE000982] [AC:AE000982:AE000782] [PN:lysophospholipase] [GN:AF1753] [OR:Archaeoglobus fulgidus] [DB:genpept-bct2] [DE:Archaeoglobus fulgidus section 125 of 172 of the complete genome.] [NT:similar to GP:1763011 percent identity: 33.46;] [LE:10776] [RE:11576] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000999_23612907_c1_696	3017	6789	144	47		
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000999_23631512_c3_1178	3018	6790	1323	440	2289	2.0e-237
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Description

gp: [GI:d1046046:g5360870] [LN:D86934] [AC:D86934] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus (strain:N315) DNA, clone\_lib:library of N31] [DB:genpept] [DE:Staphylococcus aureus genes, mec region, partial and complete cds.] [NT:ORF CN050] [LE:54760] [RE:>56082] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000999_23632883_c1_844	3019	6791	183	60		
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000999_23634682_c2_1013	3020	6792	375	124		
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000999_23634786_f3_619	3021	6793	1200	399	692	3.5e-68
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Description

gp: [GI:d1025735:g2879915] [LN:D85752] [AC:D85752] [GN:bacI] [OR:Enterococcus faecalis] [SR:Enterococcus faecalis plasmid:pPD1 DNA] [DB:genpept-bct1] [DE:Enterococcus faecalis plasmid pPD1 bacA, bacB, bacC, bacD, bacE,bacF, bacG, bacH and bacI genes, complete cds.] [LE:7732] [RE:8931] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000999_23635302_c1_867	3022	6794	138	45		
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_23635931_c1_854	3023	6795	375	124	637	2.3e-62

Description

sp: [LN:MERT\_STAAU] [AC:P08656] [GN:MERT] [OR:STAPHYLOCOCCUS AUREUS] [DE:MERCURIC TRANSPORT PROTEIN (MERCURY ION TRANSPORT PROTEIN)] [SP:P08656] [DB:swissprot]  
>pir: [LN:D29504] [AC:D29504] [PN:hypothetical 14K protein (mer operon)]  
[OR:Staphylococcus aureus] [DB:pir2] >gp: [GI:g459906] [LN:L29436]  
[AC:L29436:M15048:N00048] [GN:mert] [OR:Plasmid pI258] [SR:Plasmid pI258 DNA]  
[DB:genpept-bct1] [DE:Plasmid pI258 (from S.aureus strain RN23 8325) mercury resistance(mer) operon encoding mercuric reductase (merA), organomercuriallyase (merB), regulatory protein (merR) and membrane transportprotein (merT), complete cds.]  
[LE:2704] [RE:3090] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_23679765_f3_449	3024	6796	1269	422	1274	7.4e-130

Description

gp: [GI:e1299582:g3687416] [LN:BLY17554] [AC:Y17554] [PN:arginine deiminase] [GN:arcA]  
[OR:Bacillus licheniformis] [DB:genpept-bct1] [EC:3.5.3.6] [DE:Bacillus licheniformis arcA, arcB, arcC and arcD genes.] [LE:248] [RE:1489] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_23703175_c3_1103	3025	6797	135	44		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_23704502_f1_158	3026	6798	267	88		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_23834461_f3_588	3027	6799	162	53		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_23860812_f2_403	3028	6800	603	200	540	4.5e-52

Description

gp: [GI:g4185302] [LN:AF089862] [AC:AF089862] [PN:type-I signal peptidase SipB]  
[GN:sipB] [OR:Staphylococcus carnosus] [DB:genpept-bct2] [DE:Staphylococcus carnosus type-I signal peptidase SipA (sipA) and type-I signal peptidase SipB (sipB) genes, complete cds; and unknown gene.] [NT:leader peptidase] [LE:1502] [RE:2071] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_23866566_c2_1067	3029	6801	159	52		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_23959802_c1_787	3030	6802	171	56		

Description

NO-HIT

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_23959802_c3_1250	3031	6803	153	50		

Description

NO-HIT

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_23959802_c3_1261	3032	6804	132	43		

Description

NO-HIT

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_23959802_f2_313	3033	6805	210	69		

Description

NO-HIT

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_23959802_f3_447	3034	6806	141	46		

Description

NO-HIT

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_24016062_f1_168	3035	6807	129	42		

Description

NO-HIT

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_24023300_c2_964	3036	6808	516	171	760	2.2e-75

Description

sp: [LN:DNAA\_STAAU] [AC:P49994] [GN:DNAA] [OR:STAPHYLOCOCCUS AUREUS] [DE:CHROMOSOMAL  
 REPLICATION INITIATOR PROTEIN DNAA] [SP:P49994] [DB:swissprot] >pir: [LN:JC5607]  
 [AC:JC5607] [PN:replication initiation protein dnaA] [GN:dnaA] [CL:replication  
 initiation protein dnaA] [OR:Staphylococcus aureus] [DB:pir2]  
 >gp: [GI:d1014451:g1694677] [LN:D89066] [AC:D89066] [PN:DnaA] [GN:dnaA]  
 [OR:Staphylococcus aureus] [SR:Staphylococcus aureus DNA] [DB:genpept-bct1]  
 [DE:Staphylococcus aureus DNA for DnaA, complete cds.] [LE:456] [RE:1817] [DI:direct]

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_24101587_f3_455	3037	6809	339	112	79	0.0098

Description

pir: [LN:S42040] [AC:S42040] [PN:hypothetical protein 3] [OR:Leuconostoc oenos] [DB:pir2] >gp: [GI:g515739] [LN:LEUORF15X] [AC:L28806] [FN:unknown] [OR:Oenococcus oeni] [DB:genpept-bct1] [DE:Leuconostoc oenos complete ORF1-ORF5.] [NT:ORF3; putative] [LE:2571] [RE:2975] [DI:direct] >gp: [GI:g454968] [LN:LOPLORFG] [AC:Z29976] [OR:Oenococcus oeni] [DB:genpept-bct1] [DE:L.oenos plasmid p4028 ORF1, ORF2, ORF3, ORF4, ORF5 genes.] [NT:ORF3] [LE:2571] [RE:2975] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_24110635_c3_1231	3038	6810	132	43		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_24220062_c3_1104	3039	6811	285	94	68	0.045

Description

gp: [GI:g4731269] [LN:AF110706] [AC:AF110706] [PN:cytochrome oxidase I] [OR:Mitochondrion Bemisia tabaci] [SR:sweet potato whitefly] [DB:genpept-inv2] [DE:Bemisia tabaci cytochrome oxidase I gene, partial cds;mitochondrial gene for mitochondrial product.] [NT:premature stop codon.] [LE:<1] [RE:330] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_24234562_c2_890	3040	6812	222	73	64	0.026

Description

gp: [GI:g4808591] [LN:AF093829] [AC:AF093829] [PN:alpha-1,2-fucosyltransferase long form] [OR:Helicobacter pylori] [DB:genpept-bct2] [DE:Helicobacter pylori strain UA1182 alpha-1,2-fucosyltransferase gene, alternative products, complete cds.] [NT:ribosomal slippage] [LE:141:573] [RE:573:1042] [DI:directJoin]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_24250010_c3_1271	3041	6813	225	74		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_24255312_f1_128	3042	6814	159	52		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_24256437_c1_717	3043	6815	141	46		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_24273442_f1_22	3044	6816	384	127	144	4.1e-10

Description

pir:[LN:C70043] [AC:C70043] [PN:hypothetical protein yvlA] [GN:yvlA] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1186201:g2636026] [LN:BSUB0018] [AC:Z99121:AL009126] [GN:yvlA] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.] [LE:207957] [RE:208283] [DI:complement] >gp:[GI:e1184419:g2636039] [LN:BSUB0019] [AC:Z99122:AL009126] [GN:yvlA] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.] [LE:10417] [RE:10743] [DI:complement] >gp:[GI:g2618844] [LN:AF017113] [AC:AF017113] [PN:YvlA] [GN:yvlA] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis 300-304 degree genomic sequence.] [LE:19550] [RE:19876] [DI:direct] >gp:[GI:e1184419:g2636039] [LN:BSUB0019] [AC:Z99122:AL009126] [GN:yvlA] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept] [DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.] [LE:10417] [RE:10743] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_24273442_f1_85	3045	6817	384	127	142	6.7e-10

Description

pir:[LN:C70043] [AC:C70043] [PN:hypothetical protein yvlA] [GN:yvlA] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1186201:g2636026] [LN:BSUB0018] [AC:Z99121:AL009126] [GN:yvlA] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.] [LE:207957] [RE:208283] [DI:complement] >gp:[GI:e1184419:g2636039] [LN:BSUB0019] [AC:Z99122:AL009126] [GN:yvlA] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.] [LE:10417] [RE:10743] [DI:complement] >gp:[GI:g2618844] [LN:AF017113] [AC:AF017113] [PN:YvlA] [GN:yvlA] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis 300-304 degree genomic sequence.] [LE:19550] [RE:19876] [DI:direct] >gp:[GI:e1184419:g2636039] [LN:BSUB0019] [AC:Z99122:AL009126] [GN:yvlA] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept] [DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.] [LE:10417] [RE:10743] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_24297050_c2_904	3046	6818	141	46		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_24299037_c3_1238	3047	6819	255	84	68	0.045

Description

gp:[GI:g4049677] [LN:AF063866] [AC:AF063866] [PN:ORF MSV084 hypothetical protein] [GN:MSV084] [OR:Melanoplus sanguinipes entomopoxvirus] [DB:genpept-vrl] [DE:Melanoplus sanguinipes entomopoxvirus, complete genome.] [LE:80206] [RE:80577] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_24329192_c2_986	3048	6820	180	59		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_24332641_c1_768	3049	6821	129	42		

Description

NO-HIT

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_24401712_c1_826	3050	6822	1125	374	117	0.0014

Description

pir: [LN:C70168] [AC:C70168] [PN:DNA polymerase I (polA) homolog] [OR: *Borrelia burgdorferi*] [SR:, Lyme disease spirochete] [DB:pir2] >gp: [GI:g2688462] [LN:AE001156] [AC:AE001156:AE000783] [PN:DNA polymerase I (polA)] [GN:BB0548] [OR: *Borrelia burgdorferi*] [SR:Lyme disease spirochete] [DB:genpept-bct2] [DE: *Borrelia burgdorferi* (section 42 of 70) of the complete genome.] [NT:similar to GB:L42023 SP:P43741 PID:1005915] [LE:6171] [RE:8897] [DI:complement]

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_24406311_c3_1111	3051	6823	135	44		

Description

NO-HIT

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_24406338_c3_1122	3052	6824	186	61		

Description

NO-HIT

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_24407313_c2_880	3053	6825	126	41		

Description

NO-HIT

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_24407812_c3_1182	3054	6826	771	256	1062	2.2e-107

Description

gp: [GI:d1046030:g5360854] [LN:D86934] [AC:D86934] [PN:glycerophosphoryldiester phosphodiesterase] [OR: *Staphylococcus aureus*] [SR: *Staphylococcus aureus* (strain:N315) DNA, clone\_lib:library of N31] [DB:genpept] [DE: *Staphylococcus aureus* genes, mec region, partial and complete cds.] [NT:ORF N039; putative] [LE:46160] [RE:>46792] [DI:complement]

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_24407828_c3_1230	3055	6827	2013	670	157	2.1e-07

Description

gp: [GI:g4049717] [LN:AF063866] [AC:AF063866] [PN:ORF MSV156 hypothetical protein] [GN:MSV156] [OR: *Melanoplus sanguinipes* entomopoxvirus] [DB:genpept-vrl] [DE: *Melanoplus sanguinipes* entomopoxvirus, complete genome.] [LE:140126] [RE:143509] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_24409452_c3_1294	3056	6828	432	143	132	7.6e-09

Description

sp: [LN:Y577\_METJA] [AC:Q57997] [GN:MJ0577] [OR:METHANOCOCCUS JANNASCHII] [DE:PROTEIN MJ0577] [SP:Q57997] [DB:swissprot] >pir:[LN:A64372] [AC:A64372] [PN:hypothetical protein homolog MJ0577] [CL:Escherichia coli ybdQ protein] [OR:Methanococcus jannaschii] [DB:pir2] [MP:FOR512975-513463] >gp:[GI:g1591284] [LN:U67506] [AC:U67506:L77117] [PN:conserved hypothetical protein] [GN:MJ0577] [OR:Methanococcus jannaschii] [DB:genpept-bct2] [DE:Methanococcus jannaschii section 48 of 150 of the complete genome.] [NT:similar to SP:P42297 PID:603780 PID:849027] [LE:8204] [RE:8692] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_24411262_f1_37	3057	6829	180	59		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_24412507_f2_339	3058	6830	135	44		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_24414680_c1_843	3059	6831	1287	428	141	1.3e-05

Description

gp:[GI:g1041785] [LN:PYU36927] [AC:U36927] [PN:rhoptry protein] [FN:erythrocyte invasion and possible binding] [OR:Plasmodium yoelii] [DB:genpept-inv1] [DE:Plasmodium yoelii rhoptry protein gene, partial cds.] [LE:<1] [RE:7206] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_24414818_f3_516	3060	6832	441	146	94	0.00083

Description

sp: [LN:PHNB\_ECOLI] [AC:P16681] [GN:PHNB] [OR:ESCHERICHIA COLI] [DE:PHNB PROTEIN] [SP:P16681] [DB:swissprot] >pir:[LN:C35718] [AC:C35718:S56335:B65220] [PN:phnB protein] [GN:phnB] [OR:Escherichia coli] [DB:pir2] >gp:[GI:g147195] [LN:ECOPHNAQ] [AC:J05260] [OR:Escherichia coli] [SR:E.coli (strain B) DNA] [DB:genpept-bct1] [DE:E.coli psiD locus containing alkylphosphonate uptake (phn) genes A through Q, complete cds.] [NT:phnB protein] [LE:3767] [RE:4210] [DI:direct] >gp:[GI:g536951] [LN:ECOUW93] [AC:U14003] [GN:phnB] [OR:Escherichia coli] [DB:genpept-bct1] [DE:Escherichia coli K-12 chromosomal region from 92.8 to 00.1 minutes.] [LE:16226] [RE:16669] [DI:complement] >gp:[GI:g1790546] [LN:AE000483] [AC:AE000483:U00096] [PN:orf, hypothetical protein] [GN:phnB] [FN:orf; Unknown] [OR:Escherichia coli] [DB:genpept-bct2] [DE:Escherichia coli K-12 MG1655 section 373 of 400 of the complete genome.] [NT:f147; 100 pct identical amino acid sequence and] [LE:97] [RE:540] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000999_24424092_c2_1017	3061	6833	522	173	104	0.00027
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**Description**

gp: [GI:e1488089:g5051453] [LN:NME242841] [AC:AJ242841] [PN:hypothetical protein] [OR:Neisseria meningitidis] [DB:genpept-bct1] [DE:Neisseria meningitidis DNA for opaA region, strain Z2491.] [NT:ORFA] [LE:10162] [RE:10707] [DI:direct]  
>gp: [GI:e1488089:g5051453] [LN:NME242841] [AC:AJ242841] [PN:hypothetical protein] [OR:Neisseria meningitidis] [DB:genpept] [DE:Neisseria meningitidis DNA for opaA region, strain Z2491.] [NT:orfA] [LE:10162] [RE:10707] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000999_24430392_c1_856	3062	6834	681	226	1116	4.1e-113
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**Description**

sp: [LN:MERB\_STAAU] [AC:P08653] [GN:MERB] [OR:STAPHYLOCOCCUS AUREUS] [EC:4.99.1.2] [DE:ALKYLMERCURY LYASE, (ORGANOMERCURIAL LYASE)] [SP:P08653] [DB:swissprot]  
>pir: [LN:F29504] [AC:F29504] [PN:alkylmercury lyase,] [CL:alkylmercury lyase] [OR:Staphylococcus aureus] [EC:4.99.1.2] [DB:pir2] >gp: [GI:g459908] [LN:L29436] [AC:L29436:M15048:N00048] [PN:organomercurial lyase] [GN:merB] [OR:Plasmid pI258] [SR:Plasmid pI258 DNA] [DB:genpept-bct1] [DE:Plasmid pI258 (from S.aureus strain RN23 8325) mercury resistance(mer) operon encoding mercuric reductase (merA), organomercuriallyase (merB), regulatory protein (merR) and membrane transportprotein (merT), complete cds.] [LE:4873] [RE:5523] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000999_24431502_c3_1121	3063	6835	846	281	347	1.3e-31
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**Description**

gp: [GI:g3818562] [LN:AF076529] [AC:AF076529] [PN:ATP binding protein BviA] [GN:bviA] [OR:Butyrivibrio fibrisolvans] [DB:genpept-bct2] [DE:Butyrivibrio fibrisolvans response regulator homolog gene, partialcds; histidine kinase homolog, butyrivibriocin AR10 operon, complete sequence; and unknown gene.] [LE:2342] [RE:3187] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000999_24432662_c2_1052	3064	6836	969	322	301	2.3e-47
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**Description**

sp: [LN:YACK\_ECOLI] [AC:P36649:P75655] [GN:YACK] [OR:ESCHERICHIA COLI] [DE:PROBABLE 53.4 KD BLUE-COPPER PROTEIN YACQ PRECURSOR] [SP:P36649:P75655] [DB:swissprot]  
>pir: [LN:C64735] [AC:C64735:S45200] [PN:probable copper-binding protein yack] [GN:yack] [OR:Escherichia coli] [DB:pir2] >gp: [GI:g1786314] [LN:AE000121] [AC:AE000121:U00096] [PN:orf, hypothetical protein] [GN:yacK] [FN:orf; Unknown] [OR:Escherichia coli] [DB:genpept-bct2] [DE:Escherichia coli K-12 MG1655 section 11 of 400 of the completestgenome.] [NT:o516; 100 pct identical to 463 residues] [LE:9364] [RE:10914] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000999_24475252_f1_1	3065	6837	159	52		
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**Description**

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503000999_24486008_c2_1059	3066	6838	978	325	136	1.6e-06
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Description

gp: [GI:g4378164] [LN:AF102543] [AC:AF102543] [PN:unknown] [OR:Zymomonas mobilis] [DB:genpept-bct2] [DE:Zymomonas mobilis 5,10-methylenetetrahydrofolate reductase (metF) gene, partial cds; lipoprotein precursor (vacJ), ferredoxin-NADP+reductase (fpr), succinic semialdehyde dehydrogenase (gabD), thymidylate synthetase (thyA), gluconate permease (gntP), UTP-glucose-1-phosphate uridyltransferase, diaminopimedatedecarboxylase (lysA), arginosuccinate lyase (argH), NADH-dependentbutanol dehydrogenase (yugJ), and morphine 6-dehydrogenase (mdh) genes, complete cds; tRNA-Ala gene, complete sequence; aminopeptidase N (pepN) gene, complete cds; and unknown genes.] [NT:zm4orf2] [LE:12502] [RE:13458] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503000999_24641941_f3_456	3067	6839	510	169		
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503000999_24645817_c2_979	3068	6840	453	150	461	1.0e-43
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Description

gp: [GI:g143421] [LN:BACRG] [AC:M57623:J05723] [PN:ribosomal protein L9] [GN:ribosomal protein L9] [OR:Bacillus stearothermophilus] [SR:B.stearothermophilus DNA] [DB:genpept-bct1] [DE:B.stearothermophilus ribosomal protein L9 gene, complete cds.] [LE:1] [RE:450] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503000999_24647142_c2_930	3069	6841	645	214	575	8.7e-56
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Description

gp: [GI:e352094:g2462707] [LN:SXLACRPH] [AC:Y14599] [PN:hypothetical protein] [GN:orf5] [OR:Staphylococcus xylosus] [DB:genpept-bct1] [DE:Staphylococcus xylosus lacR, lacP, lacH genes and 2 ORF's.] [LE:6476] [RE:7105] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503000999_24647292_f3_668	3070	6842	1275	424	1180	6.7e-120
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Description

sp: [LN:PBUX\_BACSU] [AC:P42086] [GN:PBUX] [OR:BACILLUS SUBTILIS] [DE:XANTHINE PERMEASE] [SP:P42086] [DB:swissprot] >pir:[LN:S51310] [AC:S51310:E69673] [PN:xanthine permease pbuX] [GN:pbuX] [CL:xanthine permease pbuX] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:g1256618] [LN:BACYACA] [AC:L77246] [PN:transport protein] [GN:ypaQ] [FN:pyrimidine salvage] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis (YAC10-9 clone) DNA region between the serA and kdg loci.] [NT:26% of identity to the Bacillus caldolyticus uracil] [LE:2007] [RE:3323] [DI:direct] >gp: [GI:e1183652:g2634625] [LN:BSUB0012] [AC:Z99115:AL009126] [PN:xanthine permease] [GN:pbuX] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 12 of 21): from 2195541 to 2409220.] [NT:alternate gene name: ypaQ] [SP:P42086] [LE:121829] [RE:123145] [DI:complement] >gp: [GI:g633170] [LN:BSXPTPBUX] [AC:X83878] [PN:xanthine permease] [GN:pbuX] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis xpt and pbuX genes.] [SP:P42086] [LE:938] [RE:2254] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_24650427_f3_493	3071	6843	3126	1041	1653	2.3e-220

Description

pir:[LN:F64114] [AC:F64114] [PN:type I site-specific deoxyribonuclease, chain hsdR] [GN:hsdR] [CL:DEAD/H box helicase homology] [OR:Haemophilus influenzae] [EC:3.1.21.3] [DB:pir2] >gp:[GI:g1574743] [LN:U32808] [AC:U32808:L42023] [PN:type I restriction enzyme (hsdR)] [GN:HI1285] [OR:Haemophilus influenzae Rd] [DB:genpept-bct2] [DE:Haemophilus influenzae Rd section 123 of 163 of the complete genome.] [NT:similar to PID:1685100 percent identity: 59.01;] [LE:5702] [RE:8869] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_24783462_c2_1016	3072	6844	339	112	77	0.0086

Description

gp:[GI:g2772544] [LN:STREMM40G] [AC:L46817] [PN:M-40 protein] [GN:emm40] [FN:antiphagocytic] [OR:Streptococcus pyogenes] [DB:genpept-bct2] [DE:Streptococcus pyogenes M-40 protein (emm40) gene, partial cds.] [LE:<1] [RE:>341] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_24797126_f1_88	3073	6845	249	82	69	0.036

Description

gp:[GI:g2772603] [LN:DMU85764] [AC:U85764] [PN:accessory gland protein Acp32CD] [GN:Acp32CD] [FN:responsible for physiological and behavioral] [OR:Drosophila melanogaster] [SR:fruit fly] [DB:genpept-inv1] [DE:Drosophila melanogaster accessory gland protein Acp32CD (Acp32CD) gene, partial cds.] [LE:74] [RE:>377] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_24800412_c2_981	3074	6846	147	48		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_24812927_f2_227	3075	6847	183	60		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_24817142_c1_764	3076	6848	1947	648	3147	0.0

Description

pir:[LN:A40585] [AC:A40585:A35406:S54711:A42295:S36024] [PN:DNA topoisomerase (ATP-hydrolyzing), chain B] [GN:gyrB] [CL:DNA topoisomerase (ATP-hydrolyzing) chain B] [OR:Staphylococcus aureus] [EC:5.99.1.3] [DB:pir1] >gp:[GI:g296395] [LN:SAGYRREC] [AC:X71437] [PN:DNA gyrase] [GN:gyrB] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:S.aureus genes gyrB, gyrA and recF (partial).] [SP:P20832] [LE:282] [RE:2216] [DI:direct] >gp:[GI:d1001841:g540541] [LN:STAGYRABA] [AC:D10489] [PN:DNA gyrase B] [GN:gyrB] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus (strain:ATCC12600) DNA] [DB:genpept-bct1] [EC:5.99.1.3] [DE:Staphylococcus aureus genes for DNA gyrase A and B, complete cds.] [LE:181] [RE:2115] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_24847250_f2_320	3077	6849	153	50		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_24848452_c3_1175	3078	6850	792	263	223	1.7e-18

Description

pir:[LN:H70089] [AC:H70089] [PN:hypothetical protein yycI] [GN:yycI] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:d1011959:g1064811] [LN:BACGNTZA] [AC:D78193] [GN:yycI] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:168) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis 36kb sequence between gntZ and trnY genes encoding 34 ORFs.] [LE:31210] [RE:32052] [DI:complement] >gp:[GI:e1184764:g2636585] [LN:BSUB0021] [AC:Z99124:AL009126] [GN:yycI] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 21 of 21): from 3999281 to 4214814.] [LE:149594] [RE:150436] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_254527_c2_1038	3079	6851	186	61		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_25548452_f1_207	3080	6852	915	304	354	2.3e-32

Description

pir:[LN:A69867] [AC:A69867] [PN:conserved hypothetical protein ykuT] [GN:ykuT] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1181925:g2632241] [LN:BS16829KB] [AC:AJ222587] [PN:YkuT protein] [GN:ykuT] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis 29kB DNA fragment from ykwC gene to cse15 gene.] [LE:25580] [RE:26383] [DI:complement] >gp:[GI:e1185011:g2633792] [LN:BSUB0008] [AC:Z99111:AL009126] [GN:ykuT] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 8 of 21): from 1394791 to 1603020.] [NT:similar to hypothetical proteins] [LE:95836] [RE:96639] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_25554012_c2_912	3081	6853	213	70		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_25554675_c3_1094	3082	6854	927	308	179	2.5e-11

Description

sp:[LN:SR40\_YEAST] [AC:P32583] [GN:SRP40:YKR092C:YKR412A] [OR:SACCHAROMYCES CEREVISIAE] [SR:,BAKER'S YEAST] [DE:SUPPRESSOR PROTEIN SRP40] [SP:P32583] [DB:swissprot] >pir:[LN:S38170] [AC:S38170:S40645:S37702] [PN:SRP40 protein:protein YKR092c:protein YKR412a] [GN:SRP40] [OR:Saccharomyces cerevisiae] [DB:pir2] [MP:11R] >gp:[GI:g450552] [LN:SCDNACHXI] [AC:X73541] [OR:Saccharomyces cerevisiae] [SR:baker's yeast] [DB:genpept-pln1] [DE:S.cerevisiae DNA of chromosome XI, right arm.] [NT:ORF YKR412] [SP:P32583] [LE:1952] [RE:3172] [DI:complement] >gp:[GI:g486581] [LN:SCYKR092C] [AC:Z28317:Y13137] [GN:SRP40] [OR:Saccharomyces cerevisiae] [SR:baker's yeast] [DB:genpept-pln1] [DE:S.cerevisiae chromosome XI reading frame ORF YKR092c.] [NT:ORF YKR092c] [SP:P32583] [LE:400] [RE:1620] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_25565637_f2_257	3083	6855	126	41		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_25583568_f1_12	3084	6856	363	120	71	0.022

Description

pir: [LN:T03326] [AC:T03326] [PN:gene 119 protein] [GN:119] [OR:Lactococcus phage bIL170] [DB:pir2] >gp: [GI:g3282279] [LN:AF009630] [AC:AF009630] [PN:119] [GN:119] [OR:bacteriophage bIL170] [DB:genpept-phg] [DE:Bacteriophage bIL170, complete genome.] [LE:15351] [RE:15644] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_25587802_c1_809	3085	6857	777	258	114	0.00010

Description

sp: [LN:FLIZ\_BORB] [AC:Q44904:Q44764] [GN:FLIZ:BB0276] [OR:BORRELIA BURGDORFERI] [SR:, LYME DISEASE SPIROCHETE] [DE:FLAGELLAR PROTEIN FLIZ] [SP:Q44904:Q44764] [DB:swissprot] >pir: [LN:D70134] [AC:D70134] [PN:flagellar biosynthesis protein (fliz) homolog] [OR:Borrelia burgdorferi] [SR:, Lyme disease spirochete] [DB:pir2] >gp: [GI:g1165261] [LN:BBU43739] [AC:U43739] [PN:Fliz] [GN:fliz] [OR:Borrelia burgdorferi] [SR:Lyme disease spirochete strain=B31] [DB:genpept-bct1] [DE:Borrelia burgdorferi fesmid clone 31, complete sequence.] [NT:flagellar protein required for flagella formation] [LE:9847] [RE:10473] [DI:complement] >gp: [GI:g2688190] [LN:AE001137] [AC:AE001137:AE000783] [PN:flagellar biosynthesis protein (fliz)] [GN:BB0276] [OR:Borrelia burgdorferi] [SR:Lyme disease spirochete] [DB:genpept-bct2] [DE:Borrelia burgdorferi (section 23 of 70) of the complete genome.] [NT:similar to PID:1165261 PID:1185058 SP:Q44904] [LE:15237] [RE:15863] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_25642038_f3_481	3086	6858	138	45		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_25660880_c2_975	3087	6859	177	58		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_25667767_c3_1114	3088	6860	1191	396	907	5.7e-91

Description

pir: [LN:B69847] [AC:B69847] [PN:cystathionine beta-lyase homolog yjcJ] [GN:yjcJ] [CL:O-succinylhomoserine (thiol)-lyase] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1183208:g2633542] [LN:BSUB0007] [AC:Z99110:AL009126] [GN:yjcJ] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 7 of 21): from 1194391 to 1411140.] [NT:similar to cystathionine beta-lyase] [LE:64687] [RE:65859] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_25679712_f3_626	3089	6861	660	219	153	2.0e-09

Description

gp: [GI:e1315386:g3417427] [LN:SPBC30B4] [AC:AL031262] [PN:hypothetical protein]  
 [GN:SPBC30B4.01c] [OR:Schizosaccharomyces pombe] [SR:fission yeast] [DB:genpept-pln1]  
 [DE:S.pombe chromosome II cosmid c30B4.] [NT:SPBC30B4.01c, len:344aa, similarity,  
 YNL283C,] [LE:<1] [RE:1034] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_25792911_c1_777	3090	6862	129	42		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_25831512_c3_1105	3091	6863	129	42		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_26172675_f1_124	3092	6864	129	42		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_26181512_c2_1003	3093	6865	126	41		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_26198535_c3_1116	3094	6866	765	254	136	5.4e-07

Description

pir: [LN:D70817] [AC:D70817] [PN:hypothetical protein Rv1716] [GN:Rv1716]  
 [OR:Mycobacterium tuberculosis] [DB:pir2] >gp: [GI:e1299966:g3261548] [LN:MTV048]  
 [AC:AL022003:AL123456] [PN:hypothetical protein Rv1716] [GN:Rv1716] [OR:Mycobacterium  
 tuberculosis] [DB:genpept-bct1] [DE:Mycobacterium tuberculosis H37Rv complete genome;  
 segment 77/162.] [NT:Rv1716, (MTV048.03,MTCY04C12.01) len: 276. Unknown] [LE:1750]  
 [RE:2580] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_26214002_f3_647	3095	6867	870	289	627	2.7e-61

Description

sp: [LN:SP0J\_BACSU] [AC:P26497] [GN:SP00J] [OR:BACILLUS SUBTILIS] [DE:STAGE 0 SPORULATION PROTEIN J] [SP:P26497] [DB:swissprot] >pir:[LN:A38536] [AC:I40445:A38536:S66020:E69710:S18081] [PN:Soj antagonist / chromosome positioning and transport protein spo0J:spo0J93 protein:stage 0 sporulation protein J93] [GN:spo0J:spo0J93] [CL:Bacillus subtilis transport protein spo0J] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:d1005768:g467380] [LN:BAC180K] [AC:D26185] [PN:stage 0 sporulation] [GN:spo0J] [OR:Bacillus subtilis] [SR:Bacillus subtilis (sub\_species:Marburg, strain:168) DNA] [DB:genpept-bct1] [DE:B. subtilis DNA, 180 kilobase region of replication origin.] [LE:53552] [RE:54400] [DI:complement] >gp:[GI:g40031] [LN:BSORIGS] [AC:X62539] [GN:spo0J93] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B. subtilis genes rpmH, rnpA, 50kd, gidA and gidB.] [SP:P26497] [LE:9000] [RE:9848] [DI:direct] >gp:[GI:e1184822:g2636643] [LN:BSUB0021] [AC:Z99124:AL009126] [PN:antagonist of Soj] [GN:spo0J] [FN:involved in positionning part of the chromosome] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 21 of 21): from 3999281 to 4214814.] [SP:P26497] [LE:205484] [RE:206332] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_26261512_f2_275	3096	6868	162	53		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_26351510_f2_375	3097	6869	138	45		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_26365911_f1_165	3098	6870	561	186	203	2.3e-16

Description

pir: [LN:E69779] [AC:E69779] [PN:transcription regulator TetR/AcrR family homolog ydeS] [GN:ydeS] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:d1020119:g1881339] [LN:AB001488] [AC:AB001488] [GN:ydeS] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:168) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis genome sequence, 148 kb sequence of the region between 35 and 47 degree.] [NT:PROBABLE TRANSCRIPTIONAL REGULATOR, SIMILAR TO] [LE:111555] [RE:112151] [DI:direct] >gp:[GI:e1182498:g2632832] [LN:BSUB0003] [AC:Z99106:AL009126] [GN:ydeS] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 3 of 21): from 402751 to 611850.] [NT:similar to transcriptional regulator (TetR/AcrR) [LE:175301] [RE:175897] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_26597010_f3_530	3099	6871	186	61	103	2.9e-05

Description

sp: [LN:Y4UH\_RHISN] [AC:Q53200] [GN:Y4UH] [OR:RHIZOBIUM SP] [SR:NGR234,] [DE:PUTATIVE INSERTION SEQUENCE ATP-BINDING PROTEIN Y4UH] [SP:Q53200] [DB:swissprot] >gp: [GI:e213893:g1486429] [LN:RSPNGR234] [AC:Z68203] [PN:transposase homologue] [GN:orf10] [OR:Rhizobium sp.] [SR:Rhizobium sp] [DB:genpept-bct1] [DE:Rhizobium sp. plasmid NGR234a DNA.] [NT:putative] [SP:Q53200] [LE:13370] [RE:14116] [DI:complement] >gp: [GI:g2182658] [LN:AE000099] [AC:AE000099:U00090] [PN:Y4uH] [GN:y4uH] [OR:Rhizobium sp. NGR234] [DB:genpept-bct2] [DE:Rhizobium sp. NGR234 plasmid pNGR234a, section 36 of 46 of thecomplete plasmid sequence.] [NT:putative insertion sequence ATP-binding protein] [LE:8181] [RE:8927] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_26600015_f1_162	3100	6872	354	117	280	1.6e-24

Description

sp: [LN:RNPA\_BACSU] [AC:P25814] [GN:RNPA] [OR:BACILLUS SUBTILIS] [EC:3.1.26.5] [DE:RIBONUCLEASE P PROTEIN COMPONENT, (PROTEIN C5) (RNASE P)] [SP:P25814] [DB:swissprot] >pir: [LN:S66029] [AC:S66029:D69693] [PN:ribonuclease P protein component rnpA] [GN:rnpA] [CL:ribonuclease P, protein component] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:d1005777:g467389] [LN:BAC180K] [AC:D26185] [PN:protein component of ribonuclease P] [GN:rnpA] [OR:Bacillus subtilis] [SR:Bacillus subtilis (sub\_species:Marburg, strain:168) DNA] [DB:genpept-bct1] [DE:B. subtilis DNA, 180 kilobase region of replication origin.] [LE:62749] [RE:63099] [DI:complement] >gp: [GI:e1184831:g2636652] [LN:BSUB0021] [AC:Z99124:AL009126] [PN:ribonuclease P (protein component)] [GN:rnpA] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:3.1.26.5] [DE:Bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.] [SP:P25814] [LE:214681] [RE:215031] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_26604502_f2_390	3101	6873	159	52	205	1.4e-16

Description

sp: [LN:RL34\_BACST] [AC:P23376] [GN:RPMH] [OR:BACILLUS STEAROTHERMOPHILUS] [DE:50S RIBOSOMAL PROTEIN L34] [SP:P23376] [DB:swissprot] >pir: [LN:C48396] [AC:C48396] [PN:ribosomal protein L34] [CL:Escherichia coli ribosomal protein L34] [OR:Bacillus stearothermophilus] [DB:pir2]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_26615636_f1_194	3102	6874	144	47		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_26756660_c2_950	3103	6875	651	216	109	0.00035

Description

pir: [LN:B69858] [AC:B69858] [PN:hypothetical protein yknW] [GN:yknW] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1185024:g2633805] [LN:BSUB0008] [AC:Z99111:AL009126] [GN:yknW] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.] [LE:108197] [RE:108892] [DI:direct] >gp: [GI:g3282118] [LN:AF012285] [AC:AF012285:AF012284:U51911] [PN:YknW] [GN:yknW] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis mobA-nprE gene region.] [LE:8685] [RE:9380] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_26759707_c1_830	3104	6876	450	149	504	2.9e-48

Description

gp: [GI: d1046006:g5360830] [LN: D86934] [AC: D86934] [OR: *Staphylococcus aureus*] [SR: *Staphylococcus aureus* (strain: N315) DNA, clone\_lib: library of N31] [DB: genpept] [DE: *Staphylococcus aureus* genes, mec region, partial and complete cds.] [NT: ORF N044] [LE: 28947] [RE: 29264] [DI: direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_270890_c3_1162	3105	6877	186	61		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_2745462_c1_691	3106	6878	642	213	116	0.00066

Description

gp: [GI: e1407824:g4493894] [LN: PFMAL3P2] [AC: AL034558] [GN: MAL3P2.16] [OR: *Plasmodium falciparum*] [SR: malaria parasite *P. falciparum*] [DB: genpept-inv1] [DE: *Plasmodium falciparum* MAL3P2, complete sequence.] [NT: predicted using hexExon; MAL3P2.16 (PF0235w),] [LE: 73132:73647] [RE: 73149:77270] [DI: directJoin]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_2782563_c3_1129	3107	6879	153	50		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_2819632_f1_105	3108	6880	387	128		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_2867812_c2_1060	3109	6881	213	70		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_2921941_c1_680	3110	6882	159	52		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_2925292_f2_325	3111	6883	123	40		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_2931557_c3_1158	3112	6884	1119	372	1692	3.7e-174

Description

sp: [LN:RECF\_STAAU] [AC:P29232] [GN:RECF] [OR:STAPHYLOCOCCUS AUREUS] [DE:RECF PROTEIN] [SP:P29232] [DB:swissprot] >pir: [LN:C40585] [AC:S54710:C40585:C42295:S36023] [PN:recF protein] [CL:recF protein] [OR:Staphylococcus aureus] [DB:pir2]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000999_29320127_c3_1181	3113	6885	390	129	677	1.4e-66
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Description

gp: [GI:d1046033:g5360857] [LN:D86934] [AC:D86934] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus (strain:N315) DNA, clone\_lib:library of N31] [DB:genpept] [DE:Staphylococcus aureus genes, mec region, partial and complete cds.] [NT:ORF CN041] [LE:47629] [RE:>48018] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000999_2946092_c2_1006	3114	6886	435	144	97	0.00051
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Description

pir: [LN:F71224] [AC:F71224] [PN:hypothetical protein PH0057] [GN:PH0057] [CL:protein kinase C inhibitor:histidine triad homology] [OR:Pyrococcus horikoshii] [DB:pir2] >gp: [GI:d1030068:g3256442] [LN:AP000001] [AC:AP000001:AB009465:AB009464:AB009466:AB009467:AB009468:AB009469] [PN:168aa long hypothetical protein] [GN:PH0057] [OR:Pyrococcus horikoshii] [SR:Pyrococcus horikoshii (strain:OT3) DNA] [DB:genpept-bct1] [DE:Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt. position (1/7).] [NT:similar to owl:HPAE00058613 percent identity:] [LE:49752] [RE:50258] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000999_29532926_c3_1128	3115	6887	156	51		
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000999_29860902_c3_1115	3116	6888	2277	758	1816	2.7e-187
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Description

pir: [LN:C69657] [AC:C69657] [PN:cobalamin-independent methionine synthase metC] [GN:metC] [CL:cobalamin-independent methionine synthase] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1181518:g2632038] [LN:BSAJ2571] [AC:AJ002571] [PN:MetC] [GN:metC] [FN:involved in methionine metabolism] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis 168 56 kb DNA fragment between xlyA and ykoR.] [SP:P80877] [LE:35445] [RE:37733] [DI:complement] >gp: [GI:e1183338:g2633672] [LN:BSUB0007] [AC:Z99110:AL009126] [PN:cobalamin-independent methionine synthase] [GN:metC] [FN:methionine biosynthesis] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 7 of 21): from 1194391 to 1411140.] [SP:P80877] [LE:188394] [RE:190682] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000999_3007887_f1_113	3117	6889	129	42		
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_30080255_f1_172	3118	6890	384	127		

Description

NO-HIT

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_30084637_f3_567	3119	6891	156	51		

Description

NO-HIT

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_30086682_c2_1041	3120	6892	732	243	1134	5.1e-115

Description

pir:[LN:C29504] [AC:C29504] [PN:hypothetical 24K protein (mer operon)]  
[OR:Staphylococcus aureus] [DB:pir2] >gp:[GI:g459905] [LN:L29436]  
[AC:L29436:M15048:N00048] [OR:Plasmid pI258] [SR:Plasmid pI258 DNA] [DB:genpept-bct1]  
[DE:Plasmid pI258 (from S.aureus strain RN23 8325) mercury resistance(mer) operon  
encoding mercuric reductase (merA), organomercuriallyase (merB), regulatory protein  
(merR) and membrane transportprotein (merT), complete cds.] [NT:ORF4] [LE:1936]  
[RE:2616] [DI:direct]

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_30111718_c2_1051	3121	6893	2124	707	1980	7.5e-211

Description

sp:[LN:COPB\_ENTHR] [AC:P05425] [GN:COPB] [OR:ENTEROCOCCUS HIRAE] [EC:3.6.1.36]  
[DE:COPPER/POTASSIUM-TRANSPORTING ATPASE B,] [SP:P05425] [DB:swissprot]  
>pir:[LN:B45995] [AC:B45995] [PN:copper-transporting ATPase, copB] [GN:copB]  
[CL:Enterococcus copper-transporting ATPase copB: ATPase nucleotide-binding domain  
homology:ATPase transduction domain homology] [OR:Enterococcus hirae] [EC:3.6.1.-]  
[DB:pir1] >gp:[GI:g290643] [LN:ENECPOMP] [AC:L13292:J02729] [PN:ATPase] [GN:copB]  
[FN:copper pump] [OR:Enterococcus hirae] [SR:Enterococcus hirae DNA] [DB:genpept-bct1]  
[DE:Enterococcus hirae ATPase (copA) gene, complete cds; ATPase (copB) gene, complete  
cds.] [NT:putative] [LE:2273] [RE:4510] [DI:direct]

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_30516552_f1_160	3122	6894	144	47		

Description

NO-HIT

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_31267125_c3_1216	3123	6895	132	43		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_31443827_f2_419	3124	6896	510	169	563	1.6e-54

Description

sp: [LN:SSB\_BACSU] [AC:P37455] [GN:SSB] [OR:BACILLUS SUBTILIS] [DE:SINGLE-STRAND BINDING PROTEIN (SSB) (HELIX-DESTABILIZING PROTEIN)] [SP:P37455] [DB:swissprot]  
>pir: [LN:S66014] [AC:S66014:F69718] [PN:single strand DNA binding protein ssb] [GN:ssb] [CL:single-stranded DNA-binding protein: single-stranded DNA-binding protein homology] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:d1005762:g467374] [LN:BAC180K] [AC:D26185] [PN:single strand DNA binding protein] [GN:ssb] [OR:Bacillus subtilis] [SR:Bacillus subtilis (sub\_species:Marburg, strain:168) DNA] [DB:genpept-bct1] [DE:B. subtilis DNA, 180 kilobase region of replication origin.] [LE:46882] [RE:47400] [DI:complement] >gp: [GI:e1184816:g2636637] [LN:BSUB0021] [AC:Z99124:AL009126] [PN:single-strand DNA-binding protein] [GN:ssb] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.] [SP:P37455] [LE:198814] [RE:199332] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_31535626_f3_569	3125	6897	153	50		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_3158177_f2_232	3126	6898	123	40		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_32062762_c2_954	3127	6899	183	60		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_32226577_c3_1254	3128	6900	354	117	596	5.2e-58

Description

pir: [LN:B29504] [AC:B29504] [PN:hypothetical 18K protein (mer operon)] [OR:Staphylococcus aureus] [DB:pir2] >gp: [GI:g459904] [LN:L29436] [AC:L29436:M15048:N00048] [OR:Plasmid pI258] [SR:Plasmid pI258 DNA] [DB:genpept-bct1] [DE:Plasmid pI258 (from S.aureus strain RN23 8325) mercury resistance(mer) operon encoding mercuric reductase (merA), organomercuriallyase (merB), regulatory protein (merR) and membrane transportprotein (merT), complete cds.] [NT:ORF3] [LE:1454] [RE:1939] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_32423410_c1_718	3129	6901	210	69	167	1.5e-12

Description

sp: [LN:YG27\_ARCFU] [AC:O28646] [GN:AF1627] [OR:ARCHAEGLOBUS FULGIDUS] [DE:HYPOTHETICAL TRANSCRIPTIONAL REGULATOR AF1627] [SP:O28646] [DB:swissprot] >pir: [LN:B69453] [AC:B69453] [PN:repressor protein homolog] [OR:Archaeoglobus fulgidus] [DB:pir2] >gp: [GI:g2648932] [LN:AE000990] [AC:AE000990:AE000782] [PN:repressor protein] [GN:AF1627] [OR:Archaeoglobus fulgidus] [DB:genpept-bct2] [DE:Archaeoglobus fulgidus section 117 of 172 of the complete genome.] [NT:similar to GB:L77117 PID:1590997 percent identity:] [LE:7667] [RE:7882] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_32577_f3_495	3130	6902	138	45		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_3320317_f3_648	3131	6903	237	78	150	9.5e-11

Description

gp: [GI:g2109447] [LN:SPDNAARG] [AC:AF000658] [FN:unknown] [OR:Streptococcus pneumoniae] [DB:genpept-bct2] [DE:Streptococcus pneumoniae R801 tRNA-Arg gene, partial sequence, andputative serine protease (sphtra), SPSpoJ (spspoJ), initiatorprotein (spdnaa) and beta subunit of DNA polymerase III (spdnan)genes, complete cds.] [NT:ORFX] [LE:5708] [RE:5902] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_33228180_f1_192	3132	6904	243	80		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_33244187_c3_1168	3133	6905	1989	662	1592	1.5e-163

Description

sp: [LN:YYBT\_BACSU] [AC:P37484] [GN:YYBT] [OR:BACILLUS SUBTILIS] [DE:HYPOTHETICAL 74.3 KD PROTEIN IN RPLI-COTF INTERGENIC REGION] [SP:P37484] [DB:swissprot] >pir: [LN:S65976] [AC:S65976:G70088] [PN:hypothetical protein yybT] [GN:yybT] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:d1005724:g467336] [LN:BAC180K] [AC:D26185] [PN:unknown] [OR:Bacillus subtilis] [SR:Bacillus subtilis (sub\_species:Marburg, strain:168) DNA] [DB:genpept-bct1] [DE:B. subtilis DNA, 180 kilobase region of replication origin.] [LE:11639] [RE:13618] [DI:complement] >gp: [GI:e1184777:g2636598] [LN:BSUB0021] [AC:Z99124:AL009126] [GN:yybT] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.] [SP:P37484] [LE:163571] [RE:165550] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_33261588_c2_1004	3134	6906	690	229		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_33261637_c3_1237	3135	6907	543	180	79	0.0068

Description

gp: [GI:g765070] [LN:STAATL] [AC:L41499] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus (strain 8325/4) DNA] [DB:genpept-bct1] [DE:Staphylococcus aureus ORF1, partial cds, ORF2, ORF3, autolysin(atl) genes, complete cds.] [NT:ORF1] [LE:<1] [RE:249] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_33337760_c2_983	3136	6908	705	234	1191	4.6e-121

Description

gp: [GI:g5114230] [LN:AF136709] [AC:AF136709] [PN:response regulator YycF] [GN:yycF] [OR:Staphylococcus aureus] [DB:genpept] [DE:Staphylococcus aureus response regulator YycF (yycF) and histidinekinase YycG (yycG) genes, complete cds.] [LE:649] [RE:1350] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_33720053_c1_808	3137	6909	126	41		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_33790702_f3_612	3138	6910	150	49		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_33867212_f3_548	3139	6911	339	112		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_33994126_f3_633	3140	6912	144	47	47	0.045

Description

gp: [GI:g1204027] [LN:UREUREASEA] [AC:L40489] [OR:Ureaplasma urealyticum] [SR:Ureaplasma urealyticum (strain 7) DNA] [DB:genpept-bct1] [DE:Ureaplasma urealyticum strain 7 urease operon encoding ORF1, ureA,ureB, ureC, ureE, ureF, and ureG, complete cds, and ureD genes, 5'end of cds.] [NT:ORF1; Protein sequence is in conflict with the] [LE:136] [RE:468] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_34016880_f2_333	3141	6913	2028	675	3474	0.0

Description

pir: [LN:JQ0774] [AC:JQ0774] [PN:penicillin-binding protein mecA, low-affinity:penicillin-binding protein 2'] [GN:meca] [OR:Staphylococcus epidermidis] [DB:pir2] >gp: [GI:g46994] [LN:SEMECAPB] [AC:X52592] [OR:Staphylococcus epidermidis] [DB:genpept-bct1] [DE:S. epidermidis mecA gene for PBP2' (penicillin binding protein 2').] [NT:PBP2' (AA 1 - 668)] [LE:141] [RE:2147] [DI:direct] >gp: [GI:d1046026:g5360850] [LN:D86934] [AC:D86934] [PN:penicillin binding protein 2] [GN:meca] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus (strain:N315) DNA, clone\_lib:library of N31] [DB:genpept] [DE:Staphylococcus aureus genes, mec region, partial and complete cds.] [NT:ORF N058] [LE:43471] [RE:45477] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_3401887_f1_225	3142	6914	1485	494	1969	1.7e-203

Description

pir: [LN:DEBSMP] [AC:S66039:S12623:D69638] [PN:IMP dehydrogenase, :inositol-monophosphate dehydrogenase guaB] [GN:guaB] [CL:IMP dehydrogenase:CBS homology] [OR:Bacillus subtilis] [EC:1.1.1.205] [DB:pir1] >gp: [GI:d1005787:g467399] [LN:BAC180K] [AC:D26185] [PN:IMP dehydrogenase] [GN:guaB] [OR:Bacillus subtilis] [SR:Bacillus subtilis (sub\_species:Marburg, strain:168) DNA] [DB:genpept-bct1] [DE:B. subtilis DNA, 180 kilobase region of replication origin.] [LE:79515] [RE:80981] [DI:direct] >gp: [GI:e1181942:g2632276] [LN:BSUB0001] [AC:Z99104:AL009126] [PN:inositol-monophosphate dehydrogenase] [GN:guaB] [FN:GMP biosynthesis] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:1.1.1.205] [DE:Bacillus subtilis complete genome (section 1 of 21): from 1 to 213080.] [NT:alternate gene name: guaA] [SP:P21879] [LE:15913] [RE:17379] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_34023251_f2_389	3143	6915	198	65	68	0.045

Description

gp: [GI:g205733] [LN:RATNKBNT4] [AC:M21187:J03185:M18622] [OR:Rattus norvegicus] [SR:Rat testis DNA, clone rNT19] [DB:genpept-rod] [DE:Rat neuropeptin/neuromedin N gene, exon 4.] [NT:preproneuropeptin/neuromedin N] [LE:M21218.1:8:11] [RE:232:163] [DI:directJoin]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_34160260_f2_322	3144	6916	138	45		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_34178401_f3_462	3145	6917	150	49		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_34179761_c2_903	3146	6918	147	48		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_34180340_f2_398	3147	6919	711	236	609	2.2e-59

Description

gp: [GI:d1025734:g2879914] [LN:D85752] [AC:D85752] [GN:bacH] [OR:Enterococcus faecalis] [SR:Enterococcus faecalis plasmid:pPD1 DNA] [DB:genpept-bct1] [DE:Enterococcus faecalis plasmid pPD1 bacA, bacB, bacC, bacD, bacE, bacF, bacG, bacH and bacI genes, complete cds.] [LE:7148] [RE:7735] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_34182952_f3_625	3148	6920	402	133	88	0.013

Description

pir: [LN:G69850] [AC:G69850] [PN:hypothetical protein yjhA] [GN:yjhA] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1183238:g2633572] [LN:BSUB0007] [AC:Z99110:AL009126] [GN:yjhA] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 7 of 21): from 1194391 to 1411140.] [LE:94377] [RE:95018] [DI:direct] >gp: [GI:g2612890] [LN:AF015825] [AC:AF015825] [PN:putative lipoprotein] [GN:yjhA] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis 168 cotT-rapA region sequence.] [LE:8537] [RE:9178] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_34266582_c2_965	3149	6921	1158	385	1796	3.6e-185

Description

sp: [LN:DP3B\_STAAU] [AC:P50029] [GN:DNAN] [OR:STAPHYLOCOCCUS AUREUS] [EC:2.7.7.7] [DE:DNA POLYMERASE III, BETA CHAIN,] [SP:P50029] [DB:swissprot] >pir: [LN:S54708] [AC:S54708] [PN:DNA-directed DNA polymerase, III beta chain:dnaN] [GN:dnaN] [CL:DNA-directed DNA polymerase III beta chain] [OR:Staphylococcus aureus] [EC:2.7.7.7] [DB:pir1]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_34414012_f1_211	3150	6922	273	90	336	1.8e-30

Description

pir: [LN:S66013] [AC:S66013:S11368:A69701] [PN:ribosomal protein S18 (rpsR):ribosomal protein BS21] [GN:rpsR] [CL:Escherichia coli ribosomal protein S18] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:d1005761:g467373] [LN:BAC180K] [AC:D26185] [PN:ribosomal protein S18] [GN:rpsR] [OR:Bacillus subtilis] [SR:Bacillus subtilis (sub\_species:Marburg, strain:168) DNA] [DB:genpept-bct1] [DE:B. subtilis DNA, 180 kilobase region of replication origin.] [LE:46599] [RE:46844] [DI:complement] >gp: [GI:e1184815:g2636636] [LN:BSUB0021] [AC:Z99124:AL009126] [PN:ribosomal protein S18] [GN:rpsR] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 21 of 21): from 3999281 to 4214814.] [SP:P21475] [LE:198531] [RE:198776] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_34414187_c1_692	3151	6923	399	132	152	5.8e-11

Description

pir: [LN:B69778] [AC:B69778] [PN:hypothetical protein ydeH] [GN:ydeH] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:d1020108:g1881328] [LN:AB001488] [AC:AB001488] [GN:ydeH] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:168) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis genome sequence, 148 kb sequence of the region between 35 and 47 degree.] [NT:FUNCTION UNKNOWN.] [LE:100881] [RE:101327] [DI:direct] >gp: [GI:e1182486:g2632820] [LN:BSUB0003] [AC:Z99106:AL009126] [GN:ydeH] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 3 of 21): from 402751 to 611850.] [LE:164626] [RE:165072] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_34417552_f3_615	3152	6924	381	126		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_34417813_c2_985	3153	6925	807	268	851	4.9e-85

Description

pir:[LN:A70090] [AC:A70090] [PN:hypothetical protein yycJ] [GN:yycJ] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:di1011958:g1064810] [LN:BACGNTZA] [AC:D78193] [GN:yycJ] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:168) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis 36kb sequence between gntZ and trnY genesencoding 34 ORFs.] [LE:30382] [RE:31188] [DI:complement] >gp:[GI:e1184763:g2636584] [LN:BSUB0021] [AC:Z99124:AL009126] [GN:yycJ] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.] [LE:148766] [RE:149572] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_34580342_c1_730	3154	6926	771	256	802	7.7e-80

Description

pir:[LN:A70001] [AC:A70001] [PN:ABC transporter (ATP-binding protein) homolog ytsC] [GN:ytsC] [CL:ATP-binding cassette homology] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1185911:g2635522] [LN:BSUB0016] [AC:Z99119:AL009126] [GN:ytsC] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.] [NT:similar to ABC transporter (ATP-binding protein)] [LE:112638] [RE:113399] [DI:complement] >gp:[GI:g2293177] [LN:AF008220] [AC:AF008220] [PN:transporter] [GN:ytsC] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis rrnB-dnaB genomic region.] [LE:67028] [RE:67789] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_34631527_f1_20	3155	6927	834	277	609	2.2e-59

Description

gp:[GI:di1045999:g5360823] [LN:D86934] [AC:D86934] [PN:IS150-like transposase] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus (strain:N315) DNA, clone\_lib:library of N31] [DB:genpept] [DE:Staphylococcus aureus genes, mec region, partial and complete cds.] [NT:ORF N028; putative] [LE:<20180] [RE:20578] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_34643751_c1_688	3156	6928	591	196	910	2.8e-91

Description

gp:[GI:g1916316] [LN:SAU92441] [AC:U92441:X85029] [PN:alkyl hydroperoxide reductase subunit C] [GN:ahpC] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:Staphylococcus aureus alkyl hydroperoxide reductase subunit C(aphC) and subunit F (aphF) genes, complete cds.] [NT:AhpC] [LE:791] [RE:1360] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_34664700_f2_393	3157	6929	861	286	617	3.1e-60

Description

sp: [LN:YYAA\_BACSU] [AC:P37524] [GN:YYAA] [OR:BACILLUS SUBTILIS] [DE:HYPOTHETICAL 32.8 KD PROTEIN IN SPOOJ-GIDB INTERGENIC REGION] [SP:P37524] [DB:swissprot] >pir: [LN:I40442] [AC:I40442:S66023:H70083:S18078] [PN:DNA-binding protein SpoOJ-like homolog yyAA:probable DNA binding protein (replication origin region)] [GN:yyAA] [CL:Bacillus subtilis transport protein spoOJ] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:d1005771:g467383] [LN:BAC180K] [AC:D26185] [PN:DNA binding protein (probable)] [OR:Bacillus subtilis] [SR:Bacillus subtilis (sub\_species:Marburg, strain:168) DNA] [DB:genpept-bct1] [DE:B. subtilis DNA, 180 kilobase region of replication origin.] [LE:55893] [RE:56744] [DI:complement] >gp: [GI:g40028] [LN:BSORIGS] [AC:X62539] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis genes rpmH, rnpA, 50kd, gidA and gidB.] [NT:unnamed protein product] [SP:P37524] [LE:6656] [RE:7507] [DI:direct] >gp: [GI:e1184825:g2636646] [LN:BSUB0021] [AC:Z99124:AL009126] [GN:yyAA] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 21 of 21): from 3999281 to 4214814.] [NT:similar to DNA-binding protein SpoOJ-like] [SP:P37524] [LE:207825] [RE:208676] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_35157813_f2_244	3158	6930	519	172	473	5.6e-45

Description

sp: [LN:ATDA\_ECOLI] [AC:P37354] [GN:SPEG] [OR:ESCHERICHIA COLI] [EC:2.3.1.57] [DE:ACETYLTRANSFERASE (SAT)] [SP:P37354] [DB:swissprot] >gp: [GI:d1016007:g1742583] [LN:D90799] [AC:D90799:AB001340] [PN:Spermidine N1-acetyltransferase (EC 2.3.1.57)] [GN:speG] [OR:Escherichia coli] [SR:Escherichia coli (strain:K12) DNA, clone\_lib:Kohara lambda minise] [DB:genpept-bct1] [DE:E.coli genomic DNA, Kohara clone #308(35.3-35.7 min.)] [NT:ORF\_ID:o309#16; similar to [SwissProt Accession] [LE:<18154] [RE:18711] [DI:direct] >gp: [GI:d1016029:g1742606] [LN:D90800] [AC:D90800:AB001340] [PN:Spermidine N1-acetyltransferase (EC 2.3.1.57)] [GN:speG] [OR:Escherichia coli] [SR:Escherichia coli (strain:K12) DNA, clone\_lib:Kohara lambda minise] [DB:genpept-bct1] [DE:E.coli genomic DNA, Kohara clone #309(35.4-35.7 min.)] [NT:ORF\_ID:o309#16; similar to [SwissProt Accession] [LE:<14930] [RE:15487] [DI:direct] >gp: [GI:d1016031:g1742609] [LN:D90801] [AC:D90801:AB001340] [PN:Spermidine N1-acetyltransferase (EC 2.3.1.57)] [GN:speG] [OR:Escherichia coli] [SR:Escherichia coli (strain:K12) DNA, clone\_lib:Kohara lambda minise] [DB:genpept-bct1] [DE:E.coli genomic DNA, Kohara clone #310(35.7-36.0 min.)] [NT:ORF\_ID:o309#16; similar to [SwissProt Accession] [LE:<814] [RE:1371] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_35324092_c1_772	3159	6931	987	328	219	9.3e-28

Description

sp: [LN:MET2\_YEAST] [AC:P08465] [GN:MET2:YNL277W:N0615] [OR:SACCHAROMYCES CEREVISIAE] [SR:,BAKER'S YEAST] [EC:2.3.1.31] [DE:ACETYLASE)] [SP:P08465] [DB:swissprot] >pir: [LN:S63251] [AC:S63251:A27163] [PN:homoserine O-acetyltransferase,:protein N0615:protein YNL277w] [GN:MET2] [CL:homoserine acetyltransferase] [OR:Saccharomyces cerevisiae] [EC:2.3.1.31] [DB:pir2] [MP:14L] >gp: [GI:e239735:g1302344] [LN:SCYNL277W] [AC:Z71553:Y13139] [GN:MET2] [OR:Saccharomyces cerevisiae] [SR:baker's yeast] [DB:genpept-pln1] [DE:S.cerevisiae chromosome XIV reading frame ORF YNL277w.] [NT:ORF YNL277w] [SP:P08465] [LE:896] [RE:2356] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_35334686_f2_331	3160	6932	1659	552	1253	1.2e-127

Description

gp: [GI:g1022726] [LN:SHU35635] [AC:U35635] [PN:unknown] [OR:Staphylococcus haemolyticus] [SR:Staphylococcus haemolyticus strain=Y176] [DB:genpept-bct1] [DE:Staphylococcus haemolyticus IS1272 ORF1 and ORF2 genes, completecds.] [NT:ORF1] [LE:1101] [RE:1922] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_35343807_f1_220	3161	6933	237	78		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_35369052_c1_774	3162	6934	1404	467	1261	1.8e-128

Description

gp: [GI:g4416322] [LN:AF106032] [AC:AF106032] [PN:replicative helicase] [GN:dnAB] [OR:Bacillus stearothermophilus] [DB:genpept-bct2] [DE:Bacillus stearothermophilus replicative helicase (dnAB) gene, complete cds.] [NT:5'- 3' helicase; similar to Bacillus subtilis DnaC;] [LE:1] [RE:1365] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_35554635_c2_1001	3163	6935	132	43		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_35944052_c1_682	3164	6936	690	229		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_35978127_f3_661	3165	6937	777	258	559	4.3e-54

Description

sp: [LN:YWCG\_BACSU] [AC:P39605] [GN:YWCG:IPA-43D] [OR:BACILLUS SUBTILIS] [DE:HYPOTHETICAL 28.3 KD PROTEIN IN QOXD-VPR INTERGENIC REGION] [SP:P39605] [DB:swissprot] >pir:[LN:S39698] [AC:S39698:B70053] [PN:NADPH-flavin oxidoreductase homolog ywcG:protein ipa-43d] [GN:ywcG] [CL:NADPH-flavin oxidoreductase homolog] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:g413967] [LN:BSGENR] [AC:X73124] [GN:ipa-43d] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B. subtilis genomic region (325 to 333).] [SP:P39605] [LE:45340] [RE:46089] [DI:direct] >gp:[GI:e1186310:g2636346] [LN:BSUB0020] [AC:Z99123:AL009126] [GN:ywcG] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 20 of 21): from 3798401 to 4010550.] [NT:alternate gene name: ipa-43d; similar to] [SP:P39605] [LE:111873] [RE:112622] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_35984430_f2_444	3166	6938	126	41		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_35991677_c2_973	3167	6939	177	58		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_36135952_f2_327	3168	6940	1650	549	2777	4.0e-289

Description

gp:[GI:d1046002:g5360826] [LN:D86934] [AC:D86934] [PN:site-specific recombinase] [GN:ccrB] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus (strain:N315) DNA, clone\_lib:library of N31] [DB:genpept] [DE:Staphylococcus aureus genes, mec region, partial and complete cds.] [NT:ORF N037; cassette chromosome recombinase B] [LE:25508] [RE:27136] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_36147301_f3_670	3169	6941	237	78	78	0.0090

Description

sp:[LN:COTE\_BACSU] [AC:P14016] [GN:COTE] [OR:BACILLUS SUBTILIS] [DE:SPORE COAT PROTEIN E] [SP:P14016] [DB:swissprot] >pir:[LN:A31245] [AC:A31245:B69605] [PN:outer spore coat protein cotE] [GN:cotE] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:g1200225] [LN:BSCOTE] [AC:X13009] [PN:coat protein] [GN:cotE] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis cotE gene for 21kD coat protein.] [SP:P14016] [LE:390] [RE:935] [DI:direct] >gp:[GI:e1185294:g2634075] [LN:BSUB0009] [AC:Z99112:AL009126] [PN:morphogenic protein] [GN:cotE] [FN:outer coat assembly] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.] [SP:P14016] [LE:176015] [RE:176560] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_36211052_c1_855	3170	6942	1662	553	2755	8.5e-287

Description

sp:[LN:MERA\_STAAU] [AC:P08663] [GN:MERA] [OR:STAPHYLOCOCCUS AUREUS] [EC:1.16.1.1] [DE:MERCURIC REDUCTASE, (HG(II) REDUCTASE)] [SP:P08663] [DB:swissprot] >pir:[LN:E29504] [AC:E29504] [PN:mercury(II) reductase,:Hg(II) reductase:mercuric reductase] [GN:merA] [CL:Bacillus mercury(II) reductase:dihydrolipoamide dehydrogenase homology:heavy-metal-associated homology] [OR:Staphylococcus aureus] [EC:1.16.1.1] [DB:pir2] >gp:[GI:g459907] [LN:L29436] [AC:L29436:M15048:N00048] [PN:mercuric reductase] [GN:merA] [OR:Plasmid pI258] [SR:Plasmid pI258 DNA] [DB:genpept-bct1] [DE:Plasmid pI258 (from S.aureus strain RN23 8325) mercury resistance(mer) operon encoding mercuric reductase (merA), organomercuriallyase (merB), regulatory protein (merR) and membrane transportprotein (merT), complete cds.] [LE:3148] [RE:4791] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_36225427_f2_319	3171	6943	615	204		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_36226501_c2_1018	3172	6944	891	296		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_36228126_f2_392	3173	6945	1896	631	2407	6.4e-250

Description

sp: [LN:GIDA\_BACSU] [AC:P25812] [GN:GIDA] [OR:BACILLUS SUBTILIS] [DE:GLUCOSE INHIBITED DIVISION PROTEIN A] [SP:P25812] [DB:swissprot] >pir: [LN:BWBSGA] [AC:I40440:S66025:G69631:JQ1216:S18076] [PN:glucose-inhibited division protein gidA] [GN:gidA] [CL:gidA protein] [OR:Bacillus subtilis] [DB:pir1] >gp: [GI:d1005773:g467385] [LN:BAC180K] [AC:D26185] [PN:unknown] [GN:gidA] [OR:Bacillus subtilis] [SR:Bacillus subtilis (sub\_species:Marburg, strain:168) DNA] [DB:genpept-bct1] [DE:B. subtilis DNA, 180 kilobase region of replication origin.] [LE:57599] [RE:59485] [DI:complement] >gp: [GI:g40026] [LN:BSORIGS] [AC:X62539] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B. subtilis genes rpmH, rnpA, 50kd, gidA and gidB.] [NT:homologous to E.coli gidA] [SP:P25812] [LE:3915] [RE:5801] [DI:direct] >gp: [GI:e1184827:g2636648] [LN:BSUB0021] [AC:Z99124:AL009126] [PN:glucose-inhibited division protein] [GN:gidA] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.] [SP:P25812] [LE:209531] [RE:211417] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_36359761_f3_604	3174	6946	840	279	581	2.0e-56

Description

sp: [LN:YFOL\_STRTR] [AC:P96051] [OR:STREPTOCOCCUS THERMOPHILUS] [DE:(ORF1091)] [SP:P96051] [DB:swissprot] >gp: [GI:g1685111] [LN:STU58210] [AC:U58210] [OR:Streptococcus thermophilus] [SR:Streptococcus thermophilus strain=Sfi6] [DB:genpept-bct2] [DE:Streptococcus thermophilus tetrahydrofolatedehydrogenase/cyclohydrolase (fold), penicillin-binding protein 2b(pbp2b) and DNA repair and recombination protein (recM) genes,complete cds.] [NT:orf1091] [LE:1091] [RE:1927] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_36522507_f1_163	3175	6947	741	246	740	2.9e-73

Description

sp: [LN:GIDB\_BACSU] [AC:P25813] [GN:GIDB] [OR:BACILLUS SUBTILIS] [DE:GLUCOSE INHIBITED DIVISION PROTEIN B] [SP:P25813] [DB:swissprot] >pir: [LN:BWBSGB] [AC:I40441:S66024:H69631:JQ1217:S18077] [PN:glucose-inhibited division protein gidB] [GN:gidB] [CL:gidB protein] [OR:Bacillus subtilis] [DB:pir1] >gp: [GI:d1005772:g467384] [LN:BAC180K] [AC:D26185] [PN:unknown] [GN:gidB] [OR:Bacillus subtilis] [SR:Bacillus subtilis (sub\_species:Marburg, strain:168) DNA] [DB:genpept-bct1] [DE:B. subtilis DNA, 180 kilobase region of replication origin.] [LE:56866] [RE:57585] [DI:complement] >gp: [GI:g40027] [LN:BSORIGS] [AC:X62539] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B. subtilis genes rpmH, rnpA, 50kd, gidA and gidB.] [NT:homologous to E.coli gidB] [SP:P25813] [LE:5815] [RE:6534] [DI:direct] >gp: [GI:e1184826:g2636647] [LN:BSUB0021] [AC:Z99124:AL009126] [PN:glucose-inhibited division protein] [GN:gidB] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.] [SP:P25813] [LE:208798] [RE:209517] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_36584652_c1_805	3176	6948	339	112	380	4.0e-35

Description

gp: [GI:d1045996:g5360820] [LN:D86934] [AC:D86934] [PN:transposase] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus (strain:N315) DNA, clone\_lib:library of N31] [DB:genpept] [DE:Staphylococcus aureus genes, mec region, partial and complete cds.] [NT:ORF N026; putative] [LE:19527] [RE:19751] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_37892_f1_217	3177	6949	162	53		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_3906578_f1_8	3178	6950	123	40		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_3913137_f2_262	3179	6951	570	189	982	6.5e-99

Description

gp: [GI:g459909] [LN:L29436] [AC:L29436:M15048:N00048] [OR:Plasmid pI258] [SR:Plasmid pI258 DNA] [DB:genpept-bct1] [DE:Plasmid pI258 (from S.aureus strain RN23 8325) mercury resistance (mer) operon encoding mercuric reductase (merA), organomercuriallyase (merB), regulatory protein (merR) and membrane transportprotein (merT), complete cds.] [NT:ORF1] [LE:5718] [RE:6266] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_3937713_c3_1215	3180	6952	174	57		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_3938802_f2_326	3181	6953	1383	460	2306	3.2e-239

Description

gp: [GI:d1046000:g5360824] [LN:D86934] [AC:D86934] [PN:site-specific recombinase] [GN:ccrA] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus (strain:N315) DNA, clone\_lib:library of N31] [DB:genpept] [DE:Staphylococcus aureus genes, mec region, partial and complete cds.] [NT:ORF N034; cassette chromosome recombinase A] [LE:24137] [RE:25486] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_3954450_c3_1101	3182	6954	129	42		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_4016887_f1_6	3183	6955	174	57	157	2.6e-10

Description

sp: [LN:CADA\_LISMO] [AC:Q60048] [GN:CADA] [OR:LISTERIA MONOCYTOGENES] [EC:3.6.1.-] [DE:ATPASE] [SP:Q60048] [DB:swissprot] >gp: [GI:g495646] [LN:LISCADTNP] [AC:L28104] [PN:ATPase] [GN:cadA] [FN:cadmium resistance] [OR:Transposon Tn5422] [SR:Listeria monocytogenes (individual\_isolate Lm74) DNA; Transposo] [DB:genpept-una] [DE:Listeria monocytogenes ATPase (cadA) gene; accessory protein (cadC) gene; resolvase (tnpR) gene and transposase (tnpA) gene.] [LE:158] [RE:2293] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_4022952_f1_64	3184	6956	1515	504	1186	3.9e-140

Description

pir:[LN:C70880] [AC:C70880] [PN:probable hsdM protein] [GN:hsdM] [OR:Mycobacterium tuberculosis] [DB:pir2] >gp:[GI:e1173886:g2624278] [LN:MTV002] [AC:AL008967:AL123456] [PN:hsdM] [GN:hsdM] [OR:Mycobacterium tuberculosis] [DB:genpept-bct1] [DE:Mycobacterium tuberculosis H37Rv complete genome; segment 122/162.] [NT:Rv2756c, (MTV002.21c), len: 540 aa. hsdM, type I] [LE:19902] [RE:21524] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_4025302_f3_464	3185	6957	1293	430	1892	2.4e-195

Description

sp:[LN:ARSB\_STAAU] [AC:P30329] [GN:ARSB] [OR:STAPHYLOCOCCUS AUREUS] [DE:ARSENICAL PUMP MEMBRANE PROTEIN] [SP:P30329] [DB:swissprot] >pir:[LN:C41903] [AC:C41903] [PN:arsenical pump membrane protein] [GN:arsB] [CL:arsenical pump membrane protein] [OR:Staphylococcus aureus] [DB:pir1] >gp:[GI:g150728] [LN:PI2ARSRBC] [AC:M86824] [PN:arsenic efflux pump protein] [GN:arsB] [FN:arsenic efflux pump component (membrane) [OR:Plasmid pI258] [SR:Plasmid pI258 DNA] [DB:genpept-bct1] [DE:Plasmid pI258 arsenic resistance operon (arsRBC) genes, completecds.] [LE:587] [RE:1876] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_4093937_c3_1172	3186	6958	192	63		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_4098518_c2_1040	3187	6959	417	138	682	4.0e-67

Description

sp:[LN:MERR\_STAAU] [AC:P22874] [GN:MERR] [OR:STAPHYLOCOCCUS AUREUS] [DE:MERCURIC RESISTANCE OPERON REGULATORY PROTEIN] [SP:P22874] [DB:swissprot] >pir:[LN:A29504] [AC:A29504] [PN:hypothetical 16K protein (mer operon)] [CL:transcription repressor glnR] [OR:Staphylococcus aureus] [DB:pir2] >gp:[GI:g459903] [LN:L29436] [AC:L29436:M15048:N00048] [OR:Plasmid pI258] [SR:Plasmid pI258 DNA] [DB:genpept-bct1] [DE:Plasmid pI258 (from S.aureus strain RN23 8325) mercury resistance(mer) operon encoding mercuric reductase (merA), organomercuriallyase (merB), regulatory protein (merR) and membrane transportprotein (merT), complete cds.] [NT:ORF2] [LE:1030] [RE:1437] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_4120462_f2_235	3188	6960	945	314	791	1.1e-78

Description

sp:[LN:ARCL\_ECOLI] [AC:Q46807] [GN:YQEA] [OR:ESCHERICHIA COLI] [DE:CARBAMATE KINASE-LIKE PROTEIN 1] [SP:Q46807] [DB:swissprot] >pir:[LN:B65071] [AC:B65071] [PN:hypothetical protein b2874] [CL:carbamate kinase] [OR:Escherichia coli] [DB:pir2] >gp:[GI:g887824] [LN:ECU28375] [AC:U28375] [OR:Escherichia coli] [DB:genpept-bct1] [DE:Escherichia coli K-12 genome; approximately 64 to 65 minutes.] [NT:ORF\_o310] [LE:21276] [RE:22208] [DI:direct] >gp:[GI:g1789238] [LN:AE000370] [AC:AE000370:U00096] [PN:putative kinase] [GN:yqeA] [FN:putative enzyme; Not classified] [OR:Escherichia coli] [DB:genpept-bct2] [DE:Escherichia coli K-12 MG1655 section 260 of 400 of the completegenome.] [NT:o310; This 310 aa ORF is 45 pct identical (21 gaps)] [LE:11360] [RE:12292] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_41265_c3_1170	3189	6961	1365	454	1593	1.2e-163

Description

pir: [LN:A42280] [AC:S65968:A42280:H69683] [PN:adenylosuccinate synthase, purA:IMP--aspartate ligase] [GN:purA] [CL:adenylosuccinate synthase] [OR:Bacillus subtilis] [EC:6.3.4.4] [DB:pir2] >gp: [GI:d1005716:g467328] [LN:BAC180K] [AC:D26185] [PN:adenylosuccinate synthetase] [GN:purA] [OR:Bacillus subtilis] [SR:Bacillus subtilis (sub\_species:Marburg, strain:168) DNA] [DB:genpept-bct1] [DE:B. subtilis DNA, 180 kilobase region of replication origin.] [LE:3429] [RE:4721] [DI:complement] >gp: [GI:e1184768:g2636589] [LN:BSUB0021] [AC:Z99124:AL009126] [PN:adenylosuccinate synthetase] [GN:purA] [FN:AMP biosynthesis] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:6.3.4.4] [DE:Bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.] [SP:P29726] [LE:155361] [RE:156653] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_4179680_c2_977	3190	6962	936	311	214	1.7e-16

Description

sp: [LN:YYBS\_BACSU] [AC:P37485] [GN:YYBS] [OR:BACILLUS SUBTILIS] [DE:HYPOTHETICAL 34.5 KD PROTEIN IN RPLI-COTF INTERGENIC REGION] [SP:P37485] [DB:swissprot] >pir: [LN:S65977] [AC:S65977:F70088] [PN:hypothetical protein yybS] [GN:yybS] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:d1005725:g467337] [LN:BAC180K] [AC:D26185] [PN:unknown] [OR:Bacillus subtilis] [SR:Bacillus subtilis (sub\_species:Marburg, strain:168) DNA] [DB:genpept-bct1] [DE:B. subtilis DNA, 180 kilobase region of replication origin.] [LE:13655] [RE:14584] [DI:complement] >gp: [GI:e1184778:g2636599] [LN:BSUB0021] [AC:Z99124:AL009126] [GN:yybS] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.] [SP:P37485] [LE:165587] [RE:166516] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_4196051_f1_29	3191	6963	333	110	424	8.7e-40

Description

pir: [LN:A41902] [AC:A41902] [PN:arsenical resistance operon repressor] [GN:arsR] [CL:arsenical resistance operon repressor] [OR:Staphylococcus xylosus] [DB:pir1]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_42162_c3_1124	3192	6964	126	41		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_4305342_f2_445	3193	6965	1557	518	2015	2.2e-208

Description

sp: [LN:GUAA\_BACSU] [AC:P29727:O34531] [GN:GUAA] [OR:BACILLUS SUBTILIS] [EC:6.3.5.2] [DE:AMIDOTRANSFERASE] (GMP SYNTHETASE) [SP:P29727:O34531] [DB:swissprot] >pir: [LN:C69638] [AC:C69638:B42280] [PN:GMP synthase (glutamine-hydrolyzing), guaA] [GN:guaA] [CL:GMP synthase (glutamine-hydrolyzing) :trpG homology] [OR:Bacillus subtilis] [EC:6.3.5.2] [DB:pir2] >gp: [GI:g2239288] [LN:BSU51115] [AC:U51115] [PN:GMP synthetase] [GN:guaA] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis CotA (cotA), GabP (gabP), YeaB (yeaB), YeaC(yeaC), YebA (yebA), GMP synthetase (guaA) genes, complete cds, andAIR carboxylase I (purE) gene, partial cds.] [LE:9970] [RE:11511] [DI:direct] >gp: [GI:e1182615:g2632949] [LN:BSUB0004] [AC:Z99107:AL009126] [PN:GMP synthetase] [GN:guaA] [FN:GMP biosynthesis] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:6.3.5.2] [DE:Bacillus subtilis complete genome (section 4 of 21): from 600701 to 813890.] [NT:alternate gene name: guaB] [SP:P29727] [LE:91559] [RE:93100] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_4335750_f1_166	3194	6966	600	199	158	2.0e-11

Description

pir: [LN:I40868] [AC:I40868] [PN:hypothetical protein 3] [OR:Clostridium perfringens] [DB:pir2] >gp: [GI:g853809] [LN:CPNANH] [AC:X87369] [OR:Clostridium perfringens] [DB:genpept-bct1] [DE:C.perfringens nanH gene & ORF1,2,3 & 4.] [NT:ORF3] [LE:4957] [RE:5754] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_4453165_c1_862	3195	6967	537	178	202	1.8e-15

Description

gp: [GI:d1006123:g473790] [LN:ECO82K] [AC:D26562] [PN:'ORF'] [OR:Escherichia coli] [SR:Escherichia coli (sub\_strain W3110, strain K-12) (library: Kohara')] [DB:genpept-bct1] [DE:Escherichia coli genome, 2.4-4.1 min region (110,917-193,643 bp from 0 min).] [NT:'copper resistance protein copA homology'] [LE:25693] [RE:27117] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_446062_c3_1226	3196	6968	159	52	231	2.5e-19

Description

pir: [LN:A60634] [AC:A60634:C30471:S26349] [PN:probable transposase] [OR:Staphylococcus aureus] [DB:pir2] >gp: [GI:g46597] [LN:SAIS2571] [AC:X53952] [PN:transposase] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:S.aureus plasmid pSH6 DNA for insertion sequences IS257-1 and IS256.] [LE:188] [RE:862] [DI:direct] >gp: [GI:g3676452] [LN:AF051917] [AC:AF051917:L19570] [PN:putative transposase TnpE] [GN:tnpE] [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus plasmid pSK41, complete sequence.] [LE:40946] [RE:41620] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_4475050_f2_341	3197	6969	162	53	68	0.045

Description

pir: [LN:F71007] [AC:F71007] [PN:hypothetical protein PH1356] [GN:PH1356] [OR:Pyrococcus horikoshii] [DB:pir2] >gp: [GI:d1031405:g3257779] [LN:AP000006] [AC:AP000006:AB005215:AB009510:AB009511:AB009512:AB009513:AB009514] [PN:111aa long hypothetical protein] [GN:PH1356] [OR:Pyrococcus horikoshii] [SR:Pyrococcus horikoshii (strain:OT3) DNA, clone:Pyrococcus horikoshi] [DB:genpept-bct1] [DE:Pyrococcus horikoshii OT3 genomic DNA, 1166001-1485000 nt. position(6/7).] [LE:56557] [RE:56892] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_4485937_f1_10	3198	6970	1044	347	1060	3.5e-107

Description

sp: [LN:OTCC\_HAEIN] [AC:P44770] [GN:ARCB:HI0596] [OR:HAEMOPHILUS INFLUENZAE] [EC:2.1.3.3] [DE:ORNITHINE CARBAMOYLTRANSFERASE, CATABOLIC, (OTCASE)] [SP:P44770] [DB:swissprot] >pir: [LN:H64079] [AC:H64079] [PN:ornithine carbamoyltransferase,] [CL:ornithine carbamoyltransferase: aspartate/ornithine carbamoyltransferase homology] [OR:Haemophilus influenzae] [EC:2.1.3.3] [DB:pir2] >gp: [GI:g1573585] [LN:U32741] [AC:U32741:L42023] [PN:ornithine carbamoyltransferase (arcB)] [GN:HI0596] [OR:Haemophilus influenzae Rd] [DB:genpept-bct2] [DE:Haemophilus influenzae Rd section 56 of 163 of the complete genome.] [NT:similar to GB:X05637 SP:P08308 PID:45288 percent] [LE:3467] [RE:4471] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_448785_f3_518	3199	6971	927	308	408	4.3e-38

Description

sp: [LN:SOXR\_ARTSP] [AC:Q44311] [GN:SOXR] [OR:ARTHROBACTER SP] [SR:TE1826,] [DE:TRANSCRIPTIONAL REGULATOR SOXR] [SP:Q44311] [DB:swissprot] >gp: [GI:d1026865:g3116220] [LN:AB007122] [AC:AB007122] [PN:negative regulator] [OR:Arthrobacter sp.] [SR:Arthrobacter sp. (strain:TE1826) DNA] [DB:genpept-bct1] [DE:Arthrobacter sp. gene for negative regulator, sarcosine oxidase, transporter, creatinase, creatininase and transporter,complete cds.] [LE:321] [RE:1190] [DI:complement] >gp: [GI:d1010363:g1333651] [LN:ARGTE1826] [AC:D63413] [PN:regulator] [GN:soxR] [OR:Arthrobacter sp.] [SR:Arthrobacter sp. (strain:TE1826) DNA] [DB:genpept-bct1] [DE:Arthrobacter sp. gene for sarcosine oxidase, complete cds.] [LE:1539] [RE:2408] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_4694677_c1_832	3200	6972	324	107		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_4697337_f3_519	3201	6973	549	182	255	7.1e-22

Description

pir: [LN:B69978] [AC:B69978] [PN:2-nitropropane dioxygenase homolog yrpB] [GN:ypdB] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:g1934639] [LN:BSU93875] [AC:U93875] [PN:2-nitropropane dioxygenase] [GN:ypdB] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis alcohol dehydrogenase (adhB) gene, partial cds, hypothetical spore coat protein (yraF), hypothetical spore coatprotein (yraG), YraH (yraH), YraI (yraI), YraJ (yraJ), YraK (yraK), YraL (yraL), chitosanase precursor (csn), YraM (yraM), LysR-familytranscription regulator (yraN), YraO (yraO), YrpG (ypgG), RNAPolymerase sigma factor SigZ (sigZ), YrpE (ypgE), YrpD (ypgD), YrpC(ypgC) and 2-nitropropane dioxygenase (ypgB) genes, complete cds, and aminoglycoside 6-adenylyltransferase (aadK) gene, partial cds.] [NT:similar to 2-nitropropane dioxygenase of Williopsis] [LE:16473] [RE:17516] [DI:complement] >gp: [GI:e1183909:g2635125] [LN:BSUB0014] [AC:Z99117:AL009126] [GN:ypdB] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.] [NT:similar to 2-nitropropane dioxygenase] [LE:136734] [RE:137777] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_4714062_c1_759	3202	6974	135	44		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_4722338_c3_1233	3203	6975	234	77	57	0.047

Description

gp: [GI:g1354131] [LN:EHU48386] [AC:U48386] [PN:pEhS4] [GN:EhS4] [OR:Entamoeba histolytica] [DB:genpept-inv2] [DE:Entamoeba histolytica putative serine/threonine protein kinase(EhS4) gene, complete cds.] [NT:putative serine/threonine protein kinase] [LE:243:510] [RE:463:1791] [DI:directJoin]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_4725385_f1_213	3204	6976	675	224	366	1.2e-33

Description

sp: [LN:YRHP\_BACSU] [AC:O05406] [GN:YRHP] [OR:BACILLUS SUBTILIS] [DE:HYPOTHETICAL 23.4 KD PROTEIN IN AAPA-SIGV INTERGENIC REGION] [SP:O05406] [DB:swissprot] >pir: [LN:F69975] [AC:F69975] [PN:dihydrodipicolinate reductase homolog yrhP] [GN:yrhP] [CL:hypothetical protein b1798] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1183940:g2635156] [LN:BSUB0014] [AC:Z99117:AL009126] [GN:yrhP] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.] [NT:similar to dihydrodipicolinate reductase] [SP:O05406] [LE:167862] [RE:168494] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_4726555_f2_234	3205	6977	474	157	203	2.3e-16

Description

gp: [GI:g4980875] [LN:AE001717] [AC:AE001717:AE000512] [PN:arginine repressor] [GN:TM0371] [OR:Thermotoga maritima] [DB:genpept-bct2] [DE:Thermotoga maritima section 29 of 136 of the complete genome.] [NT:similar to GB:M27869 SP:P17893 PID:142450] [LE:2550] [RE:3008] [DI:direct] >gp: [GI:e1489641:g5102818] [LN:TMA132286] [AC:AJ132286] [PN:arginine repressor] [GN:argR] [FN:regulation of arginine biosynthesis genes] [OR:Thermotoga maritima] [DB:genpept] [DE:Thermotoga maritima argR gene, strain MSB8.] [LE:1] [RE:459] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_4766933_f3_490	3206	6978	129	42		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_4770028_c1_740	3207	6979	174	57		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_48412_f2_258	3208	6980	159	52	124	1.8e-07

Description

pir:[LN:H65154] [AC:H65154:S47779:S01252] [PN:probable transposase, 33.3K:hypothetical protein o283:probable transposase B] [GN:yi5B] [OR:Escherichia coli] [DB:pir2] >gp:[GI:g1789981] [LN:AE000433] [AC:AE000433:U00096] [PN:IS150 putative transposase] [GN:t150] [FN:IS, phage, Tn; Transposon-related functions] [OR:Escherichia coli] [DB:genpept-bct2] [DE:Escherichia coli K-12 MG1655 section 323 of 400 of the complete genome.] [NT:o283; 99 pct identical amino acid sequence and] [LE:1897] [RE:2748] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_4866425_f2_315	3209	6981	465	154	305	3.6e-27

Description

pir:[LN:B69978] [AC:B69978] [PN:2-nitropropane dioxygenase homolog yrpB] [GN:ypdB] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:g1934639] [LN:BSU93875] [AC:U93875] [PN:2-nitropropane dioxygenase] [GN:ypdB] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis alcohol dehydrogenase (adhB) gene, partial cds, hypothetical spore coat protein (yraF), hypothetical spore coat protein (yraG), YraH (yraH), YraI (yraI), YraJ (yraJ), YraK (yraK), YraL (yraL), chitosanase precursor (csn), YraM (yraM), LysR-family transcription regulator (yraN), YraO (yraO), YrpG (ypgG), RNAPolymerase sigma factor SigZ (sigZ), YrpE (ypgE), YrpD (ypgD), YrpC (ypgC) and 2-nitropropane dioxygenase (ypdB) genes, complete cds, and aminoglycoside 6-adenyltransferase (aadK) gene, partial cds.] [NT:similar to 2-nitropropane dioxygenase of Williopsis] [LE:16473] [RE:17516] [DI:complement] >gp:[GI:e1183909:g2635125] [LN:BSUB0014] [AC:Z99117:AL009126] [GN:ypdB] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 14 of 21): from 2599451 to 2812870.] [NT:similar to 2-nitropropane dioxygenase] [LE:136734] [RE:137777] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_4867343_c3_1210	3210	6982	2739	912	234	6.2e-16

Description

pir:[LN:G70178] [AC:G70178] [PN:exodeoxyribonuclease V, alpha chain (recD) homolog] [OR: *Borrelia burgdorferi*] [SR:, Lyme disease spirochete] [DB:pir2] >gp:[GI:g2688552] [LN:AE001164] [AC:AE001164:AE000783] [PN:exodeoxyribonuclease V, alpha chain (recD)] [GN:BB0632] [OR: *Borrelia burgdorferi*] [SR:Lyme disease spirochete] [DB:genpept-bct2] [DE: *Borrelia burgdorferi* (section 50 of 70) of the complete genome.] [NT:similar to SP:P04993 GB:X04581 GB:X04582 PID:42683] [LE:9371] [RE:11203] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_4895250_f3_627	3211	6983	180	59		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_492086_f3_540	3212	6984	1824	607		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_4957943_f3_655	3213	6985	600	199	205	7.3e-16

Description

sp: [LN:F26\_CAEEL] [AC:Q21122] [GN:K02B2.1] [OR:CAENORHABDITIS ELEGANS] [EC:2.7.1.105:3.1.3.46] [DE:BISPHOSPHATASE,] [SP:Q21122] [DB:swissprot] >gp: [GI:g1118103] [LN:CELK02B2] [AC:U41558] [GN:K02B2.1] [OR:Caenorhabditis elegans] [DB:genpept-inv2] [DE:Caenorhabditis elegans cosmid K02B2.] [NT:Contains similarity to Pfam domain: PF00300 (PGAM),] [LE:5652:5766:6320:6579] [RE:5700:5991:6527:6830] [DI:directJoin]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_4971051_c2_1028	3214	6986	825	274	196	1.3e-15

Description

gp: [GI:g1405404] [LN:LLU60336] [AC:U60336] [PN:AbiGi] [GN:abiGi] [FN:with AbiGi, causes abortive infection of phage] [OR:Lactococcus lactis subsp. cremoris] [DB:genpept-bct1] [DE:Lactococcus lactis cremoris abortive infection proteins (abiGi andabiGi) genes, complete cds.] [LE:4376] [RE:5125] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_5133462_f3_538	3215	6987	1530	509	146	1.2e-06

Description

pir: [LN:G71620] [AC:G71620] [PN:hypothetical protein PFB0195c] [GN:PFB0195c] [OR:Plasmodium falciparum] [DB:pir2] >gp: [GI:g3845121] [LN:AE001380] [AC:AE001380:AE001362] [PN:hypothetical protein] [GN:PFB0195c] [OR:Plasmodium falciparum] [SR:malaria parasite P. falciparum] [DB:genpept-inv2] [DE:Plasmodium falciparum chromosome 2, section 17 of 73 of thecomplete sequence.] [NT:predicted by GlimmerM] [LE:1011] [RE:3101] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_5190938_c3_1167	3216	6988	471	156	77	0.031

Description

sp: [LN:YH37\_HAEIN] [AC:P44301] [GN:HI1737] [OR:HAEMOPHILUS INFLUENZAE] [DE:HYPOTHETICAL PROTEIN HI1737] [SP:P44301] [DB:swissprot] >pir: [LN:E64041] [AC:E64041] [PN:branched-chain amino acid transport protein azld homolog HI1737] [CL:branched-chain amino acid transport protein azld] [OR:Haemophilus influenzae] [DB:pir2] >gp: [GI:g1574595] [LN:U32846] [AC:U32846:L42023] [PN:conserved hypothetical protein] [GN:HI1737] [OR:Haemophilus influenzae Rd] [DB:genpept-bct2] [DE:Haemophilus influenzae Rd section 161 of 163 of the complete genome.] [NT:similar to GB:AL009126 percent identity: 53.70,] [LE:9500] [RE:9829] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_5275393_f1_18	3217	6989	132	43		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_5292300_c2_1002	3218	6990	342	113	83	0.029

Description

pir:[LN:A71655] [AC:A71655] [PN:hypothetical protein RP511] [GN:RP511] [OR:Rickettsia prowazekii] [DB:pir2] >gp:[GI:e1342807:g3861063] [LN:RPXX03] [AC:AJ235272:AJ235269] [PN:unknown] [GN:RP511] [OR:Rickettsia prowazekii] [DB:genpept-bct1] [DE:Rickettsia prowazekii strain Madrid E, complete genome; segment3/4.] [LE:35291] [RE:38143] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_5313316_c2_936	3219	6991	1413	470	245	8.3e-38

Description

pir:[LN:S74046] [AC:S74046] [PN:probable sugar transport protein c0110] [OR:Sulfolobus solfataricus] [DB:pir2] >gp:[GI:e283949:g1707740] [LN:SS100KBFR] [AC:Y08256] [PN:sugar transporter] [GN:orf c01010] [OR:Sulfolobus solfataricus] [DB:genpept-bct1] [DE:S.solfataricus 100 kbp DNA fragment.] [LE:71310] [RE:72581] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_5367337_c3_1274	3220	6992	138	45		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_57217_c1_735	3221	6993	207	68		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_582777_c2_892	3222	6994	1476	491	1405	9.7e-144

Description

sp:[LN:YHCL\_BACSU] [AC:P54596] [GN:YHCL] [OR:BACILLUS SUBTILIS] [DE:HYPOTHETICAL 49.0 KD PROTEIN IN CSPB-GLPP INTERGENIC REGION] [SP:P54596] [DB:swissprot] >pir:[LN:H69822] [AC:H69822] [PN:sodium-glutamate symporter homolog yhcL] [GN:yhcL] [CL:Bacillus subtilis sodium-glutamate symporter homolog yhcL] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e233874:g1239988] [LN:BS75DGREG] [AC:X96983] [PN:hypothetical protein] [GN:yhcL] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis chromosomal DNA (region 75 degrees: cspB upstream of glpPFKD operon).] [NT:similarity to the proton/sodium-glutamate symport] [SP:P54596] [LE:7868] [RE:9259] [DI:direct] >gp:[GI:e1182902:g2633236] [LN:BSUB0005] [AC:Z99108:AL009126] [GN:yhcL] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 5 of 21): from 802821 to 1011250.] [NT:similar to sodium-glutamate symporter] [SP:P54596] [LE:183674] [RE:185065] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_595937_f2_394	3223	6995	177	58		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_6016063_f3_662	3224	6996	123	40		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_6054512_f3_600	3225	6997	207	68		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_6095000_f2_425	3226	6998	147	48		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_649141_f2_330	3227	6999	567	188		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_6521882_f1_32	3228	7000	195	64	81	0.0019

Description

gp: [GI:g5306165] [LN:AF160864] [AC:AF160864] [PN:orf98] [GN:orf98] [OR:Mitochondrion Tetrahymena pyriformis] [SR:Tetrahymena pyriformis] [DB:genpept] [DE:Tetrahymena pyriformis mitochondrial DNA, complete genome.] [NT:Open reading frame ymf71 (CPGN); ATT initiation] [LE:37598] [RE:37894] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_6643751_c1_859	3229	7001	270	89		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_6644537_f1_178	3230	7002	258	85		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_6650267_f3_611	3231	7003	123	40		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_6715_c3_1123	3232	7004	510	169		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_6728178_f1_176	3233	7005	129	42		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_6728578_c2_942	3234	7006	1893	630	678	1.1e-66

Description

pir: [LN:B70001] [AC:B70001] [PN:ABC transporter (permease) homolog ytsD] [GN:ytsD] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1185910:g2635521] [LN:BSUB0016] [AC:Z99119:AL009126] [GN:ytsD] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 16 of 21): from 2997771 to 3213410.] [NT:similar to ABC transporter (permease)] [LE:110708] [RE:112648] [DI:complement] >gp: [GI:g2293178] [LN:AF008220] [AC:AF008220] [PN:YtsD] [GN:ytsD] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis rrnB-dnaB genomic region.] [NT:similarity to NADH dehydrogenase] [LE:67779] [RE:69719] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_6819462_f1_9	3235	7007	1491	496	1508	1.2e-154

Description

gp: [GI:e1299584:g3687418] [LN:BLY17554] [AC:Y17554] [PN:permease] [GN:arcD] [OR:Bacillus licheniformis] [DB:genpept-bct1] [DE:Bacillus licheniformis arcA, arcB, arcC and arcD genes.] [LE:2579] [RE:3985] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_6828125_c1_788	3236	7008	252	83	398	5.0e-37

Description

gp: [GI:d1046032:g5360856] [LN:D86934] [AC:D86934] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus (strain:N315) DNA, clone\_lib:library of N31] [DB:genpept] [DE:Staphylococcus aureus genes, mec region, partial and complete cds.] [NT:ORF CN040] [LE:47301] [RE:>47552] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_6834501_c1_828	3237	7009	231	76		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_6929627_c2_1064	3238	7010	1146	381	756	5.7e-75

Description

pir:[LN:F70903] [AC:F70903] [PN:probable adhE protein] [GN:adhE] [CL:long-chain alcohol dehydrogenase homology] [OR:Mycobacterium tuberculosis] [DB:pir2] >gp:[GI:e322878:g2213499] [LN:MTCI28] [AC:Z97050:AL123456] [PN:adhE] [GN:adhE] [OR:Mycobacterium tuberculosis] [DB:genpept-bct1] [DE:Mycobacterium tuberculosis H37Rv complete genome; segment 10/162.] [NT:Rv0162c, (MTCI28.02c), len: 383,adhE, alcohol] [LE:1482] [RE:2633] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_6929642_f1_14	3239	7011	243	80		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_6929686_c2_1081	3240	7012	264	87	368	7.5e-34

Description

pir:[LN:A60634] [AC:A60634:C30471:S26349] [PN:probable transposase] [OR:Staphylococcus aureus] [DB:pir2] >gp:[GI:g46597] [LN:SAIS2571] [AC:X53952] [PN:transposase] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:S.aureus plasmid pSH6 DNA for insertion sequences IS257-1 and IS256.] [LE:188] [RE:862] [DI:direct] >gp:[GI:g3676452] [LN:AF051917] [AC:AF051917:L19570] [PN:putative transposase TnpE] [GN:tnpE] [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus plasmid pSK41, complete sequence.] [LE:40946] [RE:41620] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_6929686_f1_111	3241	7013	693	230	1195	1.7e-121

Description

sp:[LN:TRA2\_STAAU] [AC:P19380] [OR:STAPHYLOCOCCUS AUREUS] [DE:TRANSPOSE FOR INSERTION SEQUENCE-LIKE ELEMENT IS431MEC] [SP:P19380] [DB:swissprot] >pir:[LN:S12093] [AC:S12093:JU0116] [PN:probable transposase] [OR:Staphylococcus aureus] [DB:pir2] >gp:[GI:g46602] [LN:SAIS431M] [AC:X53818:M18438] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:S. aureus IS431mec gene associated with methicillin resistance.] [NT:putative transposase (AA 1 - 224)] [SP:P19380] [LE:272] [RE:946] [DI:direct] >gp:[GI:e1237900:g2791991] [LN:SAMECAR1I] [AC:Y14051] [PN:putative transposase] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:Staphylococcus aureus mecA, mecR1, mecI genes and ORF168, ORF142, ORF44, ORF145 and ORF224.] [NT:ORF224] [LE:8096] [RE:8770] [DI:direct] >gp:[GI:d1046034:g5360858] [LN:D86934] [AC:D86934] [PN:transposase for insertion sequence-like element] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus (strain:N315) DNA, clone\_lib:library of N31] [DB:genpept] [DE:Staphylococcus aureus genes, mec region, partial and complete cds.] [NT:ORF N062] [LE:48054] [RE:48728] [DI:direct] >gp:[GI:d1046044:g5360868] [LN:D86934] [AC:D86934] [PN:transposase for insertion sequence-like element] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus (strain:N315) DNA, clone\_lib:library of N31] [DB:genpept] [DE:Staphylococcus aureus genes, mec region, partial and complete cds.] [NT:ORF N070] [LE:53400] [RE:54074] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_7031563_c1_763	3242	7014	243	80	358	8.6e-33

Description

pir:[LN:S54709] [AC:S54709] [PN:hypothetical protein 81] [OR:Staphylococcus aureus] [DB:pir2]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_7223587_c3_1174	3243	7015	1401	466	218	4.9e-15

Description

gp:[GI:d1011960:g1064812] [LN:BACGNTZA] [AC:D78193] [GN:yyCH] [OR:Bacillus subtilis]  
 [SR:Bacillus subtilis (strain:168) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis 36kb  
 sequence between gntZ and trnY genesencoding 34 ORFs.] [LE:32039] [RE:33415]  
 [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_7297338_f1_190	3244	7016	213	70		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_791307_c3_1273	3245	7017	156	51		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_862927_c3_1289	3246	7018	195	64		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_87562_f3_550	3247	7019	162	53		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_892142_f2_249	3248	7020	198	65		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503000999_898550_f3_629	3249	7021	126	41		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_917550_c1_869	3250	7022	216	71	143	5.2e-10

Description

gp: [GI:g929968] [LN:BAU30713] [AC:U30713] [OR:Bacillus anthracis] [SR:plasmid pXO1] [DB:genpept-bct1] [DE:Bacillus anthracis Sterne toxin plasmid pXO1 right inverted repeat element (SterneR) bordering the toxin-encoding region, ORFA and truncated ORFB genes, complete cds.] [NT:ORFA; similar to B. anthracis WeyAR element ORFA;] [LE:171] [RE:491] [DI:direct] >gp: [GI:g929971] [LN:BAU30714] [AC:U30714] [OR:Bacillus anthracis] [SR:plasmid pXO1] [DB:genpept-bct1] [DE:Bacillus anthracis Weybridge A toxin plasmid pXO1 right inverted repeat element (WeyAR) bordering the toxin-encoding region, ORFA and ORFB genes, complete cds.] [NT:ORFA; similar to B. anthracis SterneR element ORFA;] [LE:171] [RE:491] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_969050_c2_1031	3251	7023	162	53		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_970077_c3_1098	3252	7024	135	44	52	0.040

Description

gp: [GI:e264333:g1050454] [LN:CHRFBFPGE] [AC:X91081] [GN:rfbP] [OR:Campylobacter hyoilei] [DB:genpept-bct1] [DE:C.hyoilei rfbF and rfbP genes.] [LE:1896] [RE:2498] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_970250_c2_1057	3253	7025	912	303	446	4.1e-42

Description

pir: [LN:E69219] [AC:E69219] [PN:conserved hypothetical protein MTH894] [GN:MTH894] [OR:Methanobacterium thermoautotrophicum] [DB:pir2] >gp: [GI:g2621989] [LN:AE000865] [AC:AE000865:AE000666] [PN:conserved protein] [GN:MTH894] [OR:Methanobacterium thermoautotrophicum] [DB:genpept-bct1] [DE:Methanobacterium thermoautotrophicum from bases 808939 to 820180(section 71 of 148) of the complete genome.] [NT:Function Code:14.01 - Unknown, Conserved protein;] [LE:4427] [RE:5410] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_970386_f1_60	3254	7026	333	110	270	5.2e-23

Description

pir: [LN:D70073] [AC:D70073] [PN:metabolite transport protein homolog yxCC] [GN:yxCC] [CL:glucose transport protein] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1184706:g2636527] [LN:BSUB0021] [AC:Z99124:AL009126] [GN:yxCC] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 21 of 21): from 3999281 to 4214814.] [NT:similar to metabolite transport protein] [LE:87516] [RE:88901] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_9765951_c1_816	3255	7027	144	47		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000999_9773385_c1_687	3256	7028	816	271	303	5.8e-27
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Description

gp: [GI:g757830] [LN:EC4HPADNA] [AC:Z37980] [PN:2-oxo-hept-3-ene-1,7-dioate hydratase] [GN:hpaH] [OR:Escherichia coli] [DB:genpept-bct1] [DE:E. coli hpa[G,R,E,D,F,H,I,X,A,B,C] genes.] [LE:4957] [RE:5760] [DI:direct] >gp: [GI:g2695682] [LN:AF036583] [AC:AF036583] [PN:2-oxo-hept-4-ene-1,7-dioate hydratase] [GN:hpcG] [OR:Escherichia coli] [DB:genpept-bct2] [DE:Escherichia coli 2-oxo-hept-4-ene-1,7-dioate hydratase (hpcG) gene, complete cds.] [NT:OHED hydratase] [LE:1] [RE:804] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000999_979178_c3_1277	3257	7029	243	80		
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000999_9792842_c1_711	3258	7030	1851	616	1480	1.1e-151
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Description

pir: [LN:C69840] [AC:C69840] [PN:conserved hypothetical protein yitJ] [GN:yitJ] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1183103:g2633437] [LN:BSUB0006] [AC:Z99109:AL009126] [GN:yitJ] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 6 of 21): from 999501 to 1209940.] [NT:similar to hypothetical proteins] [LE:178731] [RE:180569] [DI:complement] >gp: [GI:e1173535:g2145402] [LN:BSY09476] [AC:Y09476] [PN:YitJ] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B. subtilis 54kb genomic DNA fragment.] [NT:putative - Some homology with Meth2 (S. cerevisiae)] [LE:35957] [RE:37795] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000999_980000_c3_1090	3259	7031	228	75		
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503000999_9806332_f3_491	3260	7032	450	149	237	9.3e-20
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Description

pir: [LN:A71175] [AC:A71175] [PN:probable dehydrogenase] [GN:PH0597] [OR:Pyrococcus horikoshii] [DB:pir2] >gp: [GI:d1030629:g3257003] [LN:AP000002] [AC:AP000002:AB009475:AB009476:AB009477:AB009478:AB009479:AB009480] [PN:376aa long hypothetical dehydrogenase] [GN:PH0597] [OR:Pyrococcus horikoshii] [SR:Pyrococcus horikoshii (strain:OT3) DNA] [DB:genpept-bct1] [DE:Pyrococcus horikoshii OT3 genomic DNA, 287001-544000 nt. position(2/7).] [NT:similar to owl:BSZ9404317 percent identity: 49.821] [LE:248539] [RE:249669] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_9806692_c3_1251	3261	7033	1374	457	907	5.7e-91

Description

sp: [LN:YMER\_STAAU] [AC:P08655] [OR:STAPHYLOCOCCUS AUREUS] [DE:HYPOTHETICAL 19.7 KD PROTEIN IN MERCURIC RESISTANCE OPERON] [SP:P08655] [DB:swissprot] >pir:[LN:G29504] [AC:G29504] [PN:hypothetical 20K protein (mer regulatory region)] [OR:Staphylococcus aureus] [DB:pir2] >gp:[GI:g459902] [LN:L29436] [AC:L29436:M15048:N00048] [PN:regulatory protein] [GN:merR] [OR:Plasmid pI258] [SR:Plasmid pI258 DNA] [DB:genpept-bct1] [DE:Plasmid pI258 (from S.aureus strain RN23 8325) mercury resistance(mer) operon encoding mercuric reductase (merA), organomercuriallyase (merB), regulatory protein (merR) and membrane transportprotein (merT), complete cds.] [LE:188] [RE:730] [DI:direct]

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_9847811_c1_698	3262	7034	162	53		

Description

NO-HIT

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503000999_991500_f1_182	3263	7035	135	44		

Description

NO-HIT

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001000_11955055_c1_45	3264	7036	192	64		

Description

NO-HIT

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001000_1214635_c2_48	3265	7037	387	128	469	1.5e-44

Description

gp: [GI:d1036080:g4001724] [LN:AB015981] [AC:AB015981] [PN:OrfA] [GN:orfA] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus (strain:209P) DNA] [DB:genpept-bct1] [DE:Staphylococcus aureus genes for OrfA, Mnha, Mnhb, Mnhc, Mnhd, Mnhe, Mnhf and Mnhg, complete cds.] [LE:302] [RE:685] [DI:direct]

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001000_13089052_c2_46	3266	7038	123	40		

Description

NO-HIT

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001000_1378550_f3_34	3267	7039	144	47		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001000_14460932_f2_21	3268	7040	294	97	451	1.2e-42

Description

gp: [GI:g1022726] [LN:SHU35635] [AC:U35635] [PN:unknown] [OR:Staphylococcus haemolyticus] [SR:Staphylococcus haemolyticus strain=Y176] [DB:genpept-bct1] [DE:Staphylococcus haemolyticus IS1272 ORF1 and ORF2 genes, completecds.] [NT:ORF1] [LE:1101] [RE:1922] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001000_14500036_c3_66	3269	7041	129	42		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001000_15041078_f2_13	3270	7042	279	92	319	1.2e-28

Description

pir: [LN:G70012] [AC:G70012] [PN:conserved hypothetical protein yuiF] [GN:yuiF] [CL:conserved integral membrane protein HP0758] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1184283:g2635701] [LN:BSUB0017] [AC:Z99120:AL009126] [GN:yuiF] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 17 of 21): from 3197001 to 3414420.] [NT:similar to hypothetical proteins] [LE:96999] [RE:98327] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001000_21646015_f3_36	3271	7043	201	66	198	7.8e-16

Description

gp: [GI:g1022725] [LN:SHU35635] [AC:U35635] [PN:unknown] [OR:Staphylococcus haemolyticus] [SR:Staphylococcus haemolyticus strain=Y176] [DB:genpept-bct1] [DE:Staphylococcus haemolyticus IS1272 ORF1 and ORF2 genes, completecds.] [NT:ORF2] [LE:394] [RE:1083] [DI:complement] >gp: [GI:g295162] [LN:STAMECRA] [AC:L14017] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus (strain COL) DNA] [DB:genpept-bct1] [DE:Staphylococcus aureus methicillin-resistance protein (mecR) gene and unknown ORF, complete cds.] [NT:unknown ORF1; putative] [LE:1492] [RE:2181] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001000_22136087_c2_53	3272	7044	1512	503	2102	1.3e-217

Description

gp: [GI:d1036084:g4001728] [LN:AB015981] [AC:AB015981] [PN:MnhD] [GN:mnhD] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus (strain:209P) DNA] [DB:genpept-bct1] [DE:Staphylococcus aureus genes for OrfA, MnhA, MnhB, MnhC, MnhD, MnhE, MnhF and MnhG, complete cds.] [LE:3976] [RE:5472] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001000_22457312_f1_9	3273	7045	126	41		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001000_23456932_f3_26	3274	7046	153	50		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001000_23859843_f1_10	3275	7047	393	130	212	2.5e-17

Description

sp: [LN:GS13\_BACSU] [AC:P80870:005238] [GN:YUGI] [OR:BACILLUS SUBTILIS] [DE:GENERAL STRESS PROTEIN 13 (GSP13)] [SP:P80870:005238] [DB:swissprot]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001000_23947132_f3_23	3276	7048	378	125	269	2.3e-23

Description

gp: [GI:e291128:g1834379] [LN:BLCOMAB] [AC:Y10551] [GN:ComAB] [FN:positive activator of lichenysin synthetase] [OR:Bacillus licheniformis] [DB:genpept-bct1] [DE:B.licheniformis comAB gene.] [LE:617] [RE:>963] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001000_24644702_c1_41	3277	7049	435	144	647	2.0e-63

Description

gp: [GI:d1036082:g4001726] [LN:AB015981] [AC:AB015981] [PN:MnhB] [GN:mnhB] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus (strain:209P) DNA] [DB:genpept-bct1] [DE:Staphylococcus aureus genes for OrfA, MnhA, MnhB, MnhC, MnhD, MnhE, MnhF and MnhG, complete cds.] [LE:3214] [RE:3642] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001000_26756252_c3_61	3278	7050	2427	808	3318	0.0

Description

gp: [GI:d1036081:g4001725] [LN:AB015981] [AC:AB015981] [PN:MnhA] [GN:mnhA] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus (strain:209P) DNA] [DB:genpept-bct1] [DE:Staphylococcus aureus genes for OrfA, MnhA, MnhB, MnhC, MnhD, MnhE, MnhF and MnhG, complete cds.] [LE:816] [RE:3221] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001000_29742890_f2_22	3279	7051	189	62		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001000_32689812_c2_54	3280	7052	312	103	386	9.3e-36

Description

gp: [GI:d1036086:g4001730] [LN:AB015981] [AC:AB015981] [PN:MnhF] [GN:mnhF] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus (strain:209P) DNA] [DB:genpept-bct1] [DE:Staphylococcus aureus genes for OrfA, MnhA, MnhB, MnhC, MnhD, MnhE, MnhF and MnhG, complete cds.] [LE:5953] [RE:6246] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001000_33397338_c3_64	3281	7053	492	163	635	3.8e-62

Description

gp: [GI:di1036085:g4001729] [LN:AB015981] [AC:AB015981] [PN:MnhE] [GN:mnhE]  
 [OR:Staphylococcus aureus] [SR:Staphylococcus aureus (strain:209P) DNA]  
 [DB:genpept-bct1] [DE:Staphylococcus aureus genes for OrfA, Mnha, Mnhb, Mnhc, Mnhd,  
 Mnhe, Mnhf and Mnhg, complete cds.] [LE:5474] [RE:5953] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001000_34384380_c1_42	3282	7054	333	110	468	1.9e-44

Description

gp: [GI:di1036083:g4001727] [LN:AB015981] [AC:AB015981] [PN:MnhC] [GN:mnhC]  
 [OR:Staphylococcus aureus] [SR:Staphylococcus aureus (strain:209P) DNA]  
 [DB:genpept-bct1] [DE:Staphylococcus aureus genes for OrfA, Mnha, Mnhb, Mnhc, Mnhd,  
 Mnhe, Mnhf and Mnhg, complete cds.] [LE:3642] [RE:3983] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001000_34617286_t2_19	3283	7055	612	203	304	3.9e-35

Description

sp: [LN:YDJ3\_SCHPO] [AC:P87051] [GN:SPAC57A10.03] [OR:SCHIZOSACCHAROMYCES POMBE]  
 [SR:,FISSION YEAST] [EC:5.2.1.8] [DE:PROBABLE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE  
 C57A10.03,] [SP:P87051] [DB:swissprot] >gp: [GI:e313994:g2058370] [LN:SPAC57A10]  
 [AC:Z94864] [PN:peptidyl-prolyl cis-trans isomerase] [GN:SPAC57A10.03]  
 [OR:Schizosaccharomyces pombe] [SR:fission yeast] [DB:genpept-pln1] [DE:S.pombe  
 chromosome I cosmid c57A10.] [NT:SPAC57A10.03, len:155, SIMILARITY:Caenorhabditis]  
 [SP:P87051] [LE:5344:5414:5521:5779] [RE:5373:5455:5574:5858] [DI:directJoin]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001000_36604587_c1_44	3284	7056	1173	390		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001000_4017050_c3_59	3285	7057	126	41		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001000_5114680_c3_65	3286	7058	363	120	463	6.4e-44

Description

gp: [GI:di1036087:g4001731] [LN:AB015981] [AC:AB015981] [PN:MnhG] [GN:mnhG]  
 [OR:Staphylococcus aureus] [SR:Staphylococcus aureus (strain:209P) DNA]  
 [DB:genpept-bct1] [DE:Staphylococcus aureus genes for OrfA, Mnha, Mnhb, Mnhc, Mnhd,  
 Mnhe, Mnhf and Mnhg, complete cds.] [LE:6224] [RE:6580] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001000_6672886_f3_35	3287	7059	1173	390	914	1.0e-91

Description

sp: [LN:YQIG\_BACSU] [AC:P54524] [GN:YQIG] [OR:BACILLUS SUBTILIS] [EC:1.----] [DE:PROBABLE NADH-DEPENDENT FLAVIN OXIDOREDUCTASE YQIG,] [SP:P54524] [DB:swissprot] >pir: [LN:C69961] [AC:C69961] [PN:NADH-dependent flavin oxidoreductase homolog yqiG] [GN:yqiG] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:d1013261:g1303926] [LN:BACJH642] [AC:D84432:D82370] [PN:YqiG] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:JH642(trpC2 PheA1)) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis DNA, 283 Kb region containing skin element.] [LE:202096] [RE:203214] [DI:complement] >gp: [GI:e1185689:g2634855] [LN:BSUB0013] [AC:Z99116:AL009126] [GN:yqiG] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.] [NT:similar to NADH-dependent flavin oxidoreductase] [SP:P54524] [LE:120407] [RE:121525] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001000_783125_c3_56	3288	7060	183	60		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_10000312_c3_1340	3289	7061	165	54		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_10006340_f2_492	3290	7062	501	166	85	0.0011

Description

gp: [GI:g160616] [LN:PFAR45B] [AC:M83791] [PN:trophozoite antigen] [GN:R45] [OR:Plasmodium falciparum] [SR:Plasmodium falciparum (strain Tak 9.96) (library: lambda-gt11) [DB:genpept-inv1] [DE:Plasmodium falciparum trophozoite antigen gene (repeat region),partial cds.] [LE:<1] [RE:>327] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_10265677_f2_556	3291	7063	150	49		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_10267016_c2_1133	3292	7064	789	262	210	4.1e-17

Description

sp: [LN:TIPA\_STRLI] [AC:P32184] [GN:TIPA] [OR:STREPTOMYCES LIVIDANS] [DE:TRANSCRIPTIONAL ACTIVATOR TIPA] [SP:P32184] [DB:swissprot] >pir: [LN:S35354] [AC:S35354:A45923] [PN:tipA protein] [GN:tipA] [CL:tipA protein] [OR:Streptomyces lividans] [DB:pir2] >gp: [GI:g408223] [LN:S64314] [AC:S64314] [PN:TipAL-AS] [GN:tipA] [OR:Streptomyces lividans] [DB:genpept-bct1] [DE:tipAL-AS complex: tipA=TipAL-AS [Streptomyces lividans, Genomic, 1146 nt].] [NT:thiostrepton-specific recognition protein; Method:] [LE:120] [RE:881] [DI:direct] >gp: [GI:e1453008:g4808352] [LN:SCE9] [AC:AL049841] [PN:transcriptional regulator] [GN:SCE9.20] [OR:Streptomyces coelicolor] [DB:genpept-bct1] [DE:Streptomyces coelicolor cosmid E9.] [NT:SCE9.20c, tipA, transcriptional regulator, len: 253] [LE:21108] [RE:21869] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_10268818_f3_803	3293	7065	234	77		

Description

NO-HIT

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_10343756_f3_840	3294	7066	174	57		

Description

NO-HIT

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_10439005_f1_44	3295	7067	516	171	157	1.7e-11

Description

gp:[GI: d1044366:g5105267] [LN: AP000062] [AC: AP000062] [PN: 114aa long hypothetical protein] [GN: APE1580] [OR: Aeropyrum pernix] [SR: Aeropyrum pernix (strain: K1) DNA] [DB: genpept] [DE: Aeropyrum pernix genomic DNA, section 5/7.] [NT: similar to OWL: AB00946832 percent identity: 37.500] [LE: 13911] [RE: 14255] [DI: direct]

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_10548187_f3_766	3296	7068	162	53		

Description

NO-HIT

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_10581693_f2_490	3297	7069	684	227	842	4.4e-84

Description

pir:[LN: A69868] [AC: A69868] [PN: ykvJ protein] [GN: ykvJ] [CL: conserved hypothetical protein HI1191] [OR: Bacillus subtilis] [DB: pir2] > gp:[GI: e1184962:g2633743] [LN: BSUB0008] [AC: Z99111:AL009126] [GN: ykvJ] [FN: unknown] [OR: Bacillus subtilis] [DB: genpept-bct1] [DE: Bacillus subtilis complete genome (section 8 of 21): from 1394791 to 1603020.] [NT: similar to hypothetical proteins] [LE: 44124] [RE: 44783] [DI: direct]

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_10589818_f2_358	3298	7070	201	66	58	0.0051

Description

gp:[GI: e321942:g2664263] [LN: EFAS48C] [AC: Y12234] [PN: hypothetical protein] [OR: Enterococcus faecalis] [DB: genpept-bct1] [DE: E. faecalis plasmid DNA containing gene cluster involved in production and immunity to peptide antibiotic AS-48.] [NT: ORF6] [LE: 4556] [RE: 5065] [DI: direct]

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_10667002_c3_1423	3299	7071	201	66		

Description

NO-HIT

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_10667002_c3_1504	3300	7072	168	55		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_10737818_f1_230	3301	7073	471	156	223	1.7e-18

Description

sp: [LN:YP17\_LISMO] [AC:P52309] [OR:LISTERIA MONOCYTOGENES] [DE:HYPOTHETICAL 17.1 KD PROTEIN IN DNAG/DNAE 5'REGION (P17)] [SP:P52309] [DB:swissprot] >gp: [GI:g664754] [LN:LMU13165] [AC:U13165] [PN:P17] [OR:Listeria monocytogenes] [DB:genpept-bct2] [DE:Listeria monocytogenes P17 (orfP17), DNA primase (dnaG) and sigma43 subunit of RNA polymerase (rpoD) genes, complete cds.] [NT:orfP17] [LE:196] [RE:645] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_10976387_c3_1503	3302	7074	210	69		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_11023402_f3_781	3303	7075	273	90	127	2.6e-08

Description

pir: [LN:A71007] [AC:A71007] [PN:hypothetical protein PH1351] [GN:PH1351] [OR:Pyrococcus horikoshii] [DB:pir2] >gp: [GI:d1031400:g3257774] [LN:AP000006] [AC:AP000006:AB005215:AB009510:AB009511:AB009512:AB009513:AB009514] [PN:101aa long hypothetical protein] [GN:PH1351] [OR:Pyrococcus horikoshii] [SR:Pyrococcus horikoshii (strain:OT3) DNA, clone:Pyrococcus horikoshi] [DB:genpept-bct1] [DE:Pyrococcus horikoshii OT3 genomic DNA, 1166001-1485000 nt. position(6/7).] [LE:50986] [RE:51291] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_110275_f2_577	3304	7076	276	91	292	8.5e-26

Description

gp: [GI:e255528:g1617429] [LN:SEABCTS] [AC:X99127] [PN:membrane protein] [FN:iron repressible ABC transport system] [OR:Staphylococcus epidermidis] [DB:genpept-bct1] [DE:S.epidermidis gene encoding ABC transport system.] [LE:878] [RE:1624] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_11152176_c1_967	3305	7077	1029	342	1111	1.4e-112

Description

pir: [LN:A69855] [AC:A69855] [PN:low-affinity inorganic phosphate transport homolog ykaB] [GN:ykaB] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1181485:g2632005] [LN:BSAJ2571] [AC:AJ002571] [PN:YkaB] [GN:ykaB] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis 168 56 kb DNA fragment between xlyA and ykoR.] [NT:homologous to low affinity phosphate transporter] [LE:1614] [RE:2600] [DI:complement] >gp: [GI:e1183304:g2633638] [LN:BSUB0007] [AC:Z99110:AL009126] [GN:ykaB] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.] [NT:similar to low-affinity inorganic phosphate] [LE:154563] [RE:155549] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_112561_f1_99	3306	7078	138	45		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_116383_f2_590	3307	7079	165	54		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_11728376_c2_1327	3308	7080	249	82	241	2.2e-20

Description

pir: [LN:A70026] [AC:A70026] [PN:hypothetical protein yuzB] [GN:yuzB] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1184298:g2635716] [LN:BSUB0017] [AC:Z99120:AL009126] [GN:yuzB] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 17 of 21): from 3197001 to 3414420.] [LE:110425] [RE:110661] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_11831433_f2_602	3309	7081	159	52	48	0.031

Description

gp: [GI:g554799] [LN:HIVB54CH] [AC:M96497] [PN:envelope protein] [GN:env] [OR:Human immunodeficiency virus type 1] [SR:Human immunodeficiency virus type 1 (individual\_isolate ) RNA] [DB:genpept-vrl] [DE:Human immunodeficiency virus type 1 (clone B5-4) V1 & V2 regions of the envelope protein (env) gene, partial cds.] [NT:hypervariable regions V1 and V2; putative] [LE:<1] [RE:>296] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_11883557_f1_292	3310	7082	195	64		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_1199063_f1_135	3311	7083	510	169	165	5.3e-12

Description

sp: [LN:YJJP\_HAEIN] [AC:P44520] [GN:HI0108] [OR:HAEMOPHILUS INFLUENZAE] [DE:HYPOTHETICAL PROTEIN HI0108] [SP:P44520] [DB:swissprot] >pir: [LN:I64142] [AC:I64142] [PN:hypothetical protein HI0108] [OR:Haemophilus influenzae] [DB:pir2] >gp: [GI:g1573061] [LN:U32696] [AC:U32696:L42023] [PN:conserved hypothetical protein] [GN:HI0108] [OR:Haemophilus influenzae Rd] [DB:genpept-bct2] [DE:Haemophilus influenzae Rd section 11 of 163 of the complete genome.] [NT:similar to GB:U14003 SP:P39402 PID:537207 GB:U00096] [LE:4095] [RE:4988] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_1214688_f1_146	3312	7084	939	312	526	1.4e-50

Description

sp: [LN:MURB\_BACSU] [AC:P18579:P16669:P37581] [GN:MURB] [OR:BACILLUS SUBTILIS] [EC:1.1.1.158] [DE:ACETYL MURAMATE DEHYDROGENASE] [SP:P18579:P16669:P37581] [DB:swissprot] >pir: [LN:A43727] [AC:S26500:PC1128:A43727:B69662] [PN:UDP-N-acetylenolpyruvoylglucosamine reductase murB:hypothetical protein (murG 3' region)] [GN:murB] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:g142833] [LN:BACDDSA] [AC:M31827] [OR:Bacillus subtilis] [SR:Bacillus subtilis (clone: lambda-BS1) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis (clone lambda-BS1) cell division and sporulation protein (dds) gene, complete cds.] [NT:ORF2] [LE:479] [RE:1390] [DI:direct] >gp: [GI:e1185113:g2633894] [LN:BSUB0008] [AC:Z99111:AL009126] [PN:UDP-N-acetylenolpyruvoylglucosamine reductase] [GN:murB] [FN:peptidoglycan biosynthesis] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:1.1.1.158] [DE:Bacillus subtilis complete genome (section 8 of 21): from 1394791 to 1603020.] [NT:alternate gene name: ylxC] [SP:P18579] [LE:197268] [RE:198179] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_12616018_f2_357	3313	7085	270	89	84	0.0027

Description

gp: [GI:g48992] [LN:ECINCI2] [AC:X62169:S47694] [GN:pilU] [OR:Escherichia coli] [DB:genpept-bct1] [DE:E.coli IncI2 plasmid R721 pilU, plV, shf, rci genes.] [LE:29] [RE:664] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_12617827_c1_1083	3314	7086	762	253	1160	8.9e-118

Description

gp: [GI:e1393156:g4490615] [LN:SAU133520] [AC:AJ133520] [PN:triosephosphate isomerase] [GN:tpi] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:Staphylococcus aureus gap operon (gapR, gap, pgk and tpi genes).] [LE:4307] [RE:5068] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_12789077_c3_1469	3315	7087	1107	368	1311	8.9e-134

Description

sp: [LN:UVRA\_BACSU] [AC:O34863] [GN:UVRA] [OR:BACILLUS SUBTILIS] [DE:EXCINUCLEASE ABC SUBUNIT A] [SP:O34863] [DB:swissprot] >pir: [LN:F69729] [AC:F69729] [PN:excinuclease ABC chain A:excision endonuclease ABC, chain A:uvrA protein] [GN:uvrA] [CL:excinuclease ABC chain A:ATP-binding cassette homology] [OR:Bacillus subtilis] [EC:3.1.-.-] [DB:pir2] >gp: [GI:e1184422:g2636042] [LN:BSUB0019] [AC:Z99122:AL009126] [PN:excinuclease ABC (subunit A)] [GN:uvrA] [FN:excision of ultraviolet light-induced] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091 to 3809700.] [SP:O34863] [LE:12034] [RE:14907] [DI:complement] >gp: [GI:g2618842] [LN:AF017113] [AC:AF017113] [PN:excinuclease ABC subunit A] [GN:uvrA] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis 300-304 degree genomic sequence.] [LE:15386] [RE:18259] [DI:direct] >gp: [GI:e1184422:g2636042] [LN:BSUB0019] [AC:Z99122:AL009126] [PN:excinuclease ABC (subunit A)] [GN:uvrA] [FN:excision of ultraviolet light-induced] [OR:Bacillus subtilis] [DB:genpept] [DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091 to 3809700.] [SP:O34863] [LE:12034] [RE:14907] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_12929631_f2_529	3316	7088	156	51		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_12948336_c3_1475	3317	7089	273	90	316	2.4e-28

Description

sp: [LN:CLPP\_BACSU] [AC:P80244:008433] [GN:CLPP] [OR:BACILLUS SUBTILIS] [EC:3.4.21.92] [DE:(ENDOPEPTIDASE CLP) (CASEINOLYTIC PROTEASE) (PROTEASE TI)] [SP:P80244:008433] [DB:swissprot] >pir: [LN:B69601] [AC:B69601:A47683] [PN:ATP-dependent clp proteinase, chain P:stress protein G7] [GN:clpP] [CL:ATP-dependent Clp proteinase chain P] [OR:Bacillus subtilis] [EC:3.4.21.-] [DB:pir2] >gp: [GI:e1186142:g2635967] [LN:BSUB0018] [AC:Z99121:AL009126] [PN:ATP-dependent Clp protease proteolytic subunit] [GN:clpP] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:3.4.21.92] [DE:Bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.] [NT:alternate gene name: yvdN] [SP:P80244] [LE:145744] [RE:146337] [DI:direct] >gp: [GI:e313044:g1945673] [LN:BSZ94043] [AC:Z94043] [PN:hypothetical protein] [GN:yvdN] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B. subtilis genomic DNA fragment (88 kb).] [NT:similar to CLPP\_ECOLI ATP-dependent clp protease] [SP:P80244] [LE:35334] [RE:35927] [DI:complement] >gp: [GI:g2668494] [LN:BSU59754] [AC:U59754] [PN:ClpP] [GN:clpP] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis Clp protease proteolytic component (clpP) gene, complete cds.] [NT:proteolytic component of Clp protease] [LE:140] [RE:733] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_1351533_c2_1261	3318	7090	2571	856	3966	0.0

Description

sp: [LN:SECA\_STAAU] [AC:006446] [GN:SECA] [OR:STAPHYLOCOCCUS AUREUS] [DE:PREPROTEIN TRANSLOCASE SECA SUBUNIT] [SP:006446] [DB:swissprot] >gp: [GI:g2078390] [LN:SAU97062] [AC:U97062] [PN:SecA] [GN:secA] [FN:secretion] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:Staphylococcus aureus NCTC 8325 SecA (secA) gene, complete cds.] [LE:440] [RE:2971] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_1362705_c1_960	3319	7091	123	40		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_1366018_f3_723	3320	7092	135	44		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_13710887_G2_1298	3321	7093	753	250	315	3.1e-28

Description

pir:[LN:I39522] [AC:I39522] [PN:3-dehydroquinate dehydratase,, catabolic] [GN:quiB] [CL:3-dehydroquinate dehydratase:3-dehydroquinate dehydratase homology] [OR:Acinetobacter calcoaceticus] [EC:4.2.1.10] [DB:pir2] >gp:[GI:g3172120] [LN:ACCPCHAOP] [AC:L05770:U04359:M33798:U20284:U11554:L13114:L03407] [PN:catabolic dehydroquinate dehydratase] [GN:quiB] [FN:dehydration of dehydroquinate to] [OR:Acinetobacter sp. ADP1] [DB:genpept-bct2] [DE:Acinetobacter sp. ADP1 pca-qui-pob supraoperonic cluster, complete sequence.] [LE:10923] [RE:11795] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_13714193_c3_1456	3322	7094	582	193	583	1.2e-56

Description

sp:[LN:YSEA\_STACA] [AC:P47995] [OR:STAPHYLOCOCCUS CARNOSUS] [DE:HYPOTHETICAL PROTEIN IN SECA 5'REGION (ORF1) (FRAGMENT)] [SP:P47995] [DB:swissprot]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_13727318_f1_246	3323	7095	813	270	348	9.9e-32

Description

gp:[GI:g2735506] [LN:SCU96107] [AC:U96107] [PN:SceB precursor] [GN:sceB] [OR:Staphylococcus carnosus] [DB:genpept-bct2] [DE:Staphylococcus carnosus N5,N10-methylenetetrahydromethanopterinreductase homolog, SceB precursor (sceB) and putative transmembrane protein genes, complete cds, and putative Na+/H+ antiporter NhaC(nhaC) gene, partial cds.] [NT:major secreted protein] [LE:1894] [RE:2685] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_1376577_f2_374	3324	7096	675	224	77	0.0044

Description

pir:[LN:F70141] [AC:F70141] [PN:probable oligopeptide transport ATP-binding protein oppF] [GN:oppF] [CL:inner membrane protein malK:ATP-binding cassette homology] [OR:Treponema burgdorferi] [SR:, Lyme disease spirochete] [DB:pir2] >gp:[GI:g2688242] [LN:AE001140] [AC:AE001140:AE000783] [PN:oligopeptide ABC transporter, ATP-binding] [GN:BB0335] [OR:Treponema burgdorferi] [SR:Lyme disease spirochete] [DB:genpept-bct2] [DE:Treponema burgdorferi (section 26 of 70) of the complete genome.] [NT:similar to SP:P24137 percent identity: 56.81;] [LE:3216] [RE:4187] [DI:direct] >gp:[GI:g2281463] [LN:AF000366] [AC:AF000366] [PN:oligopeptide permease homolog F] [GN:oppF] [OR:Treponema burgdorferi] [SR:Lyme disease spirochete] [DB:genpept-bct2] [DE:Treponema burgdorferi oligopeptide permease homologs AI (oppAI), AII(oppAII), AIII (oppAIII), B (oppB), C (oppC), D (oppD), and F(oppF), P26 (p26) and enolase homolog (eno) genes, complete cds.] [NT:OppF] [LE:9017] [RE:9988] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_13803167_f2_373	3325	7097	552	183	157	8.0e-11

Description

pir: [LN:A69774] [AC:A69774] [PN:integrase homolog ydcL] [GN:ydcL] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:d1020071:g1881291] [LN:AB001488] [AC:AB001488] [GN:ydcL] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:168) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis genome sequence, 148 kb sequence of the region between 35 and 47 degree.] [NT:PROBABLE INTEGRASE.] [LE:62741] [RE:63847] [DI:complement] >gp: [GI:e1182446:g2632780] [LN:BSUB0003] [AC:Z99106:AL009126] [GN:ydcL] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 3 of 21): from 402751 to 611850.] [NT:similar to integrase] [LE:126486] [RE:127592] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_13834425_c2_1291	3326	7098	126	41		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_13921942_c3_1483	3327	7099	1554	517	1690	6.1e-174

Description

pir: [LN:D69675] [AC:D69675:I40024] [PN:phosphoglycerate mutase,, 2, 3-diphosphoglycerate-independent] [GN:pgm] [CL:phosphoglycerate mutase, 2, 3-bisphosphoglycerate-independent] [OR:Bacillus subtilis] [EC:5.4.2.1] [DB:pir2] >gp: [GI:e1186079:g2635904] [LN:BSUB0018] [AC:Z99121:AL009126] [PN:phosphoglycerate mutase] [GN:pgm] [FN:glycolysis] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:5.4.2.1] [DE:Bacillus subtilis complete genome (section 18 of 21): from 3399551 to 3609060.] [SP:P39773] [LE:77390] [RE:78925] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_13931527_c3_1337	3328	7100	723	240	87	0.011

Description

pir: [LN:S49604] [AC:S49604] [PN:hypothetical protein 126 (rps12 3' region)] [OR:plastid Astasia longa] [DB:pir2] >gp: [GI:e156256:g1334340] [LN:ALRPS12] [AC:X82630] [GN:orf126] [OR:Chloroplast Astasia longa] [SR:euglenophycean alga] [DB:genpept-pln1] [DE:A.longa plastid rps12, orf126 and orf288 genes.] [NT:ata start] [LE:<1424] [RE:1801] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_1408438_f1_283	3329	7101	948	315	110	8.1e-06

Description

sp: [LN:YDCZ\_ECOLI] [AC:P76111] [GN:YDCZ] [OR:ESCHERICHIA COLI] [DE:HYPOTHETICAL 15.9 KD PROTEIN IN TEHB-ANSP INTERGENIC REGION] [SP:P76111] [DB:swissprot] >pir: [LN:B64897] [AC:B64897] [PN:probable membrane protein b1447] [OR:Escherichia coli] [DB:pir2] >gp: [GI:g1787718] [LN:AE000241] [AC:AE000241:U00096] [PN:orf, hypothetical protein] [GN:b1447] [FN:orf; Unknown] [OR:Escherichia coli] [DB:genpept-bct2] [DE:Escherichia coli K-12 MG1655 section 131 of 400 of the complete genome.] [NT:f149; This 149 aa ORF is 31 pct identical (11 gaps)] [LE:9124] [RE:9573] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_14097163_f1_50	3330	7102	138	45		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_14120465_f1_56	3331	7103	513	170		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_14454632_f1_194	3332	7104	177	58	225	1.1e-18

Description

gp: [GI:g1022726] [LN:SHU35635] [AC:U35635] [PN:unknown] [OR:Staphylococcus haemolyticus] [SR:Staphylococcus haemolyticus strain=Y176] [DB:genpept-bct1] [DE:Staphylococcus haemolyticus IS1272 ORF1 and ORF2 genes, completecds.] [NT:ORF1] [LE:1101] [RE:1922] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_14460882_c1_1104	3333	7105	177	58	234	1.2e-19

Description

gp: [GI:g1022726] [LN:SHU35635] [AC:U35635] [PN:unknown] [OR:Staphylococcus haemolyticus] [SR:Staphylococcus haemolyticus strain=Y176] [DB:genpept-bct1] [DE:Staphylococcus haemolyticus IS1272 ORF1 and ORF2 genes, completecds.] [NT:ORF1] [LE:1101] [RE:1922] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_14460882_f3_776	3334	7106	183	60	128	6.0e-08

Description

gp: [GI:g1022726] [LN:SHU35635] [AC:U35635] [PN:unknown] [OR:Staphylococcus haemolyticus] [SR:Staphylococcus haemolyticus strain=Y176] [DB:genpept-bct1] [DE:Staphylococcus haemolyticus IS1272 ORF1 and ORF2 genes, completecds.] [NT:ORF1] [LE:1101] [RE:1922] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_14478377_c3_1383	3335	7107	1149	382	637	2.3e-62

Description

sp: [LN:HMPA\_BACSU] [AC:P49852] [GN:HMP:ANE3] [OR:BACILLUS SUBTILIS] [DE:FLAVOHEMOPROTEIN (HAEMOGLOBIN-LIKE PROTEIN) (FLAVOHEMOGLLOBIN)] [SP:P49852] [DB:swissprot] >pir: [LN:B69642] [AC:B69642] [PN:flavohemoglobin hmp] [GN:hmp] [CL:flavohemoglobin:cytochrome-b5 reductase homology:globin homology] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:d1011920:g1063247] [LN:BAC168TRP2] [AC:D78189] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:168trpC2) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis hmp DNA for 7 ORFs, complete cds.] [NT:high homology to flavohemoprotein (Haemoglobin-like)] [LE:999] [RE:2198] [DI:direct] >gp: [GI:e1181505:g2632025] [LN:BSAJ2571] [AC:AJ002571] [PN:YkiA] [GN:ykiA] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis 168 56 kb DNA fragment between xlyA and ykoR.] [NT:Flavohemoprotein] [SP:P49852] [LE:24916] [RE:26115] [DI:direct] >gp: [GI:e1183324:g2633658] [LN:BSUB0007] [AC:Z99110:AL009126] [PN:flavohemoglobin] [GN:hmp] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 7 of 21): from 1194391 to 1411140.] [NT:alternate gene name: ykia] [SP:P49852] [LE:177865] [RE:179064] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_14494461_c2_1178	3336	7108	168	55		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_14500052_f1_64	3337	7109	204	67		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_14538202_c3_1510	3338	7110	762	253	1034	2.0e-104

Description

sp: [LN:V296\_BACSU] [AC:P80866] [GN:YURI] [OR:BACILLUS SUBTILIS] [DE:VEGETATIVE PROTEIN 296 (VEG296)] [SP:P80866] [DB:swissprot]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_14564005_f2_456	3339	7111	249	82	87	0.0016

Description

pir: [LN:B69341] [AC:B69341] [PN:cobalt transport protein (cbiQ-1) homolog] [OR:Archaeoglobus fulgidus] [DB:pir2] >gp: [GI:g2649885] [LN:AE001054] [AC:AE001054:AE000782] [PN:cobalt transport protein (cbiQ-1)] [GN:AF0730] [OR:Archaeoglobus fulgidus] [DB:genpept-bct2] [DE:Archaeoglobus fulgidus section 53 of 172 of the complete genome.] [NT:similar to GP:1419077 percent identity: 32.61;] [LE:978] [RE:1700] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_14642203_c3_1363	3340	7112	834	277	772	1.2e-76

Description

pir: [LN:G70080] [AC:G70080] [PN:conserved hypothetical protein yxkD] [GN:yxkD] [CL:conserved hypothetical protein yitt] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1186383:g2636419] [LN:BSUB0020] [AC:Z99123:AL009126] [GN:yxkD] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 20 of 21): from 3798401 to 4010550.] [NT:similar to hypothetical proteins] [LE:188319] [RE:189155] [DI:complement] >gp: [GI:d1012387:g1783243] [LN:D83026] [AC:D83026:D45911] [GN:yxkD] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:BGSC 1A1) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis genome sequence covering lic-cel region.] [NT:homologous to jojC gene product (B. subtilis;)] [LE:35310] [RE:36146] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_14648452_c3_1464	3341	7113	801	266	346	1.6e-31

Description

gp: [GI:e244971:g1340128] [LN:SA1234] [AC:X97985] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:S.aureus orfs 1,2,3 & 4.] [NT:ORF1] [LE:537] [RE:1304] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_14875890_c3_1412	3342	7114	846	281	734	1.2e-72

Description

gp: [GI:e1359127:g4007669] [LN:SC4B5] [AC:AL034443] [PN:putative oxidoreductase] [GN:SC4B5.01c] [OR:Streptomyces coelicolor] [DB:genpept-bct1] [DE:Streptomyces coelicolor cosmid 4B5.] [NT:SC4B5.01c, probable oxidoreductase, len; 277aa,] [LE:52] [RE:885] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_14878807_f2_599	3343	7115	960	319	162	2.8e-09

Description

gp: [GI:e321943:g2664264] [LN:EFAS48C] [AC:Y12234] [PN:hypothetical protein] [OR:Enterococcus faecalis] [DB:genpept-bct1] [DE:E.faecalis plasmid DNA containing gene cluster involved in production and immunity to peptide antibiotic AS-48.] [NT:ORF7] [LE:5043] [RE:6266] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_14886052_c3_1386	3344	7116	495	164	307	2.2e-27

Description

sp: [LN:YQGC\_BACSU] [AC:P54486] [GN:YQGC] [OR:BACILLUS SUBTILIS] [DE:HYPOTHETICAL 17.3 KD PROTEIN IN CCCA-SODA INTERGENIC REGION] [SP:P54486] [DB:swissprot] >pir: [LN:G69955] [AC:G69955] [PN:hypothetical protein yqgC] [GN:yqgC] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:d1013185:g1303850] [LN:BACJH642] [AC:D84432:D82370] [PN:YqgC] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:JH642(trpC2 PheA1)) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis DNA, 283 Kb region containing skin element.] [LE:132903] [RE:133385] [DI:direct] >gp: [GI:e1185770:g2634936] [LN:BSUB0013] [AC:Z99116:AL009126] [GN:yqgC] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 13 of 21): from 2395261 to 2613730.] [SP:P54486] [LE:190236] [RE:190718] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_14970251_f3_623	3345	7117	294	97		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_15057762_c2_1198	3346	7118	1575	524	1194	2.2e-121

Description

sp: [LN:MEMP\_ALCEU] [AC:Q07252] [OR:ALCALIGENES EUTROPHUS] [DE:MEMBRANE PROTEIN] [SP:Q07252] [DB:swissprot] >pir: [LN:I39534] [AC:I39534:S33452] [PN:hypothetical protein] [OR:Alcaligenes eutrophus] [DB:pir2] >gp: [GI:g311309] [LN:AELACDEH] [AC:Z22737] [PN:putative membrane-bound protein with four times] [OR:Ralstonia eutrophus] [DB:genpept-bct1] [DE:A.eutrophus genes for lactate dehydrogenase, putative membrane-bound protein with four times repetition of Pro-Ser-Ala at the N-terminus (function unknown) and transglycosidase (partial).] [SP:Q07252] [LE:962] [RE:2503] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT17503001001_1561_c1_1025	3347	7119	1944	647	1406	7.6e-144

Description

pir: [LN:A69814] [AC:A69814] [PN:ABC transporter (ATP-binding protein) homolog yfmR] [GN:yfmR] [CL:ATP-binding cassette homology] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1182716:g2633050] [LN:BSUB0004] [AC:Z99107:AL009126] [GN:yfmR] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 4 of 21): from 600701 to 813890.] [NT:similar to ABC transporter (ATP-binding protein)] [LE:208365] [RE:210254] [DI:direct] >gp: [GI:e1182727:g2633061] [LN:BSUB0005] [AC:Z99108:AL009126] [GN:yfmR] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 5 of 21): from 802821 to 1011250.] [NT:similar to ABC transporter (ATP-binding protein)] [LE:6245] [RE:8134] [DI:direct] >gp: [GI:d1020922:g2116756] [LN:D86418] [AC:D86418] [PN:YfmR] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:AC327) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis genomic DNA 69-70 degree region, partial sequence.] [LE:2937] [RE:4826] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT17503001001_15661088_c2_1162	3348	7120	513	170		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT17503001001_15751312_f1_164	3349	7121	2136	711	1980	1.1e-204

Description

sp: [LN:ADH2\_ENTHI] [AC:Q24803:Q27649] [GN:ADH2] [OR:ENTAMOEBA HISTOLYTICA] [EC:1.1.1.1:1.2.1.10] [DE:DEHYDROGENASE, (ACDH)] [SP:Q24803:Q27649] [DB:swissprot] >gp: [GI:g488430] [LN:EHU04863] [AC:U04863] [PN:alcohol dehydrogenase 2] [OR:Entamoeba histolytica] [DB:genpept-inv1] [DE:Entamoeba histolytica HM1:IMSS alcohol dehydrogenase 2 (EhADH2)mRNA, complete cds.] [NT:The derived amino acid sequence of EhADH2 is] [LE:3] [RE:2615] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT17503001001_15752262_f3_666	3350	7122	153	50		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT17503001001_15756542_c2_1195	3351	7123	201	66		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT17503001001_157767_c3_1366	3352	7124	1077	358	534	1.9e-51

Description

gp: [GI:d1045428:g5106360] [LN:AB028629] [AC:AB028629] [PN:lipase] [GN:lipA] [OR:Clostridium perfringens] [SR:Clostridium perfringens (strain:13) DNA, clone:pSB235] [DB:genpept] [DE:Clostridium perfringens metB, cysK, ygaG, lipA genes for cystathione beta-synthase, cysteine synthase, hypothetical protein, lipase, partial and complete cds.] [NT:esterase] [LE:3248] [RE:4183] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_15781336_c2_1131	3353	7125	471	156	150	9.5e-11

Description

pir: [LN:C70059] [AC:C70059] [PN:hypothetical protein ywiB] [GN:ywiB] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1186235:g2636271] [LN:BSUB0020] [AC:Z99123:AL009126] [GN:ywiB] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 20 of 21): from 3798401 to 4010550.] [LE:35970] [RE:36398] [DI:complement] >gp: [GI:e324352:g2224755] [LN:BSZ97024] [AC:Z97024] [GN:ywiB] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis ywiA, sbo, ywiB, args and narK genes.] [LE:1255] [RE:1683] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_16522890_f1_189	3354	7126	171	56		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_16603207_f3_710	3355	7127	378	125	217	7.5e-18

Description

pir: [LN:S72776] [AC:S72776] [PN:B1496\_F1\_41 protein] [OR:Mycobacterium leprae] [DB:pir2] >gp: [GI:g466873] [LN:U00013] [AC:U00013] [PN:B1496\_F1\_41] [OR:Mycobacterium leprae] [DB:genpept-bct1] [DE:Mycobacterium leprae cosmid B1496.] [LE:29815] [RE:30312] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_166062_c2_1287	3356	7128	123	40	50	0.030

Description

pir: [LN:S73871] [AC:S73871] [PN:type I restriction enzyme ecokI specificity protein homolog:hypothetical protein H10\_orf145L:hypothetical protein H10\_orf145L] [OR:Mycoplasma pneumoniae] [SR:ATCC 29342, , ATCC 29342] [SR:ATCC 29342, ] [DB:pir2] >gp: [GI:g1674242] [LN:MPAE000053] [AC:AE000053:U00089] [GN:H10\_orf145L] [OR:Mycoplasma pneumoniae] [DB:genpept-bct2] [DE:Mycoplasma pneumoniae section 53 of 63 of the complete genome.] [NT:type I restriction enzyme ecokI specificity protein] [LE:3554] [RE:3991] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_166713_c2_1263	3357	7129	2001	666	2697	1.2e-280

Description

sp: [LN:UVRB\_BACSU] [AC:P37954:034455] [GN:UVRB:DINA:UVR] [OR:BACILLUS SUBTILIS] [DE:EXCINUCLEASE ABC SUBUNIT B (DINA PROTEIN)] [SP:P37954:034455] [DB:swissprot] >pir: [LN:G69729] [AC:G69729:I39817:B37317] [PN:excinuclease ABC chain B:DNA repair protein DinA:excision endonuclease ABC,, chain B:hypothetical protein (DNA damage-inducible A76 promoter 3' region):UrvB homolog DinA] [GN:uvrB:uvr:dinA] [CL:excinuclease ABC chain B:DEAD/H box helicase homology] [OR:Bacillus subtilis] [EC:3.1.1.-] [DB:pir2] >gp: [GI:e1184423:g2636043] [LN:BSUB0019] [AC:Z99122:AL009126] [PN:excinuclease ABC (subunit B)] [GN:uvrB] [FN:excision of ultraviolet light-induced] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091 to 3809700:] [NT:alternate gene name: dinA, uvrA] [SP:P37954] [LE:14915] [RE:16900] [DI:complement] >gp: [GI:g2618841] [LN:AF017113] [AC:AF017113] [PN:excinuclease ABC subunit B] [GN:uvrB] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis 300-304 degree genomic sequence.] [LE:13393] [RE:15378] [DI:direct] >gp: [GI:e1184423:g2636043] [LN:BSUB0019] [AC:Z99122:AL009126] [PN:excinuclease ABC (subunit B)] [GN:uvrB] [FN:excision of ultraviolet light-induced] [OR:Bacillus subtilis] [DB:genpept] [DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091 to 3809700.] [NT:alternate gene name: dinA, uvrA] [SP:P37954] [LE:14915] [RE:16900] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_16677343_c1_925	3358	7130	447	148	107	3.4e-06

Description

sp: [LN:Y357\_METJA] [AC:Q57803] [GN:MJ0357] [OR:METHANOCOCCUS JANNASCHII] [DE:HYPOTHETICAL PROTEIN MJ0357] [SP:Q57803] [DB:swissprot] >pir: [LN:E64344] [AC:E64344] [PN:hypothetical protein MJ0357] [OR:Methanococcus jannaschii] [DB:pir2] [MP:REV326407-325940] >gp: [GI:g1591066] [LN:U67489] [AC:U67489:L77117] [PN:M. jannaschii predicted coding region MJ0357] [GN:MJ0357] [OR:Methanococcus jannaschii] [DB:genpept-bct2] [DE:Methanococcus jannaschii section 31 of 150 of the complete genome.] [NT:hypothetical protein; identified by GeneMark;] [LE:1632] [RE:2099] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_16834512_c3_1401	3359	7131	1380	459	661	6.7e-65

Description

sp: [LN:PHR\_BACFI] [AC:Q04449] [GN:PHR] [OR:BACILLUS FIRMUS] [EC:4.1.99.3] [DE:(PHOTOREACTIVATING ENZYME) (FRAGMENT)] [SP:Q04449] [DB:swissprot] >gp: [GI:g142783] [LN:BACCTA] [AC:M94110] [PN:DNA photolyase] [GN:phr] [OR:Bacillus firmus] [SR:Bacillus firmus (strain OF4) DNA] [DB:genpept-bct1] [EC:4.1.99.3] [DE:Bacillus firmus DNA photolyase (phr) gene, 3' end, and cytochromeoxidase (cta) operon.] [NT:putative] [LE:1] [RE:1020] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_16850303_c1_1090	3360	7132	477	158	510	6.7e-49

Description

sp: [LN:SMPB\_BACSU] [AC:O32230] [GN:SMPB] [OR:BACILLUS SUBTILIS] [DE:SMALL PROTEIN B HOMOLOG] [SP:O32230] [DB:swissprot] >pir: [LN:F70027] [AC:F70027] [PN:conserved hypothetical protein yvaI] [GN:yvaI] [CL:small protein smpB] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1186048:g2635873] [LN:BSUB0018] [AC:Z99121:AL009126] [GN:yvaI] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 18 of 21): from 3399551 to 3609060.] [NT:similar to hypothetical proteins] [SP:O32230] [LE:50760] [RE:51230] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_17011562_c3_1354	3361	7133	168	55		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_181500_c3_1353	3362	7134	798	265	415	7.8e-39

Description

sp: [LN:TAGA\_BACSU] [AC:P27620] [GN:TAGA] [OR:BACILLUS SUBTILIS] [DE:TEICHOIC ACID BIOSYNTHESIS PROTEIN A] [SP:P27620] [DB:swissprot] >pir:[LN:B49757] [AC:B49757:B69720] [PN:polyglycerol phosphate techoic acid biosynthesis protein tagA] [GN:tagA] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:g143724] [LN:BACTAGABCD] [AC:M57497] [GN:tagA] [OR:Bacillus subtilis] [SR:B.subtilis (strain 168) DNA] [DB:genpept-bct1] [DE:B.subtilis tagA, tagB, tagC and tagD genes, complete cds.] [NT:putative] [LE:800] [RE:1570] [DI:direct] >gp:[GI:e1184481:g2636101] [LN:BSUB0019] [AC:Z99122:AL009126] [GN:tagA] [FN:polyglycerol phosphate assembly and export] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.] [SP:P27620] [LE:83340] [RE:84110] [DI:direct] >gp:[GI:e1184481:g2636101] [LN:BSUB0019] [AC:Z99122:AL009126] [GN:tagA] [FN:polyglycerol phosphate assembly and export] [OR:Bacillus subtilis] [DB:genpept] [DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.] [SP:P27620] [LE:83340] [RE:84110] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_187568_c2_1149	3363	7135	327	108	178	1.0e-13

Description

pir:[LN:F70008] [AC:F70008] [PN:hypothetical protein yufC] [GN:yufC] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1184242:g2635660] [LN:BSUB0017] [AC:Z99120:AL009126] [GN:yufC] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.] [LE:53800] [RE:54084] [DI:direct] >gp:[GI:e311513:g1934775] [LN:BSZ93932] [AC:Z93932] [PN:unknown] [GN:yufC] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis genomic DNA fragment from yufA to yufE.] [LE:7444] [RE:7728] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_187916_c2_1189	3364	7136	612	203	344	2.6e-31

Description

gp:[GI:e1314177:g3395518] [LN:PMAJ84] [AC:AJ000084] [PN:putative acetyl transferase] [GN:pat] [OR:Proteus mirabilis] [DB:genpept-bct1] [DE:Proteus mirabilis ccm and pat genes and partial ygbA gene.] [LE:949] [RE:1506] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_189187_c1_1040	3365	7137	132	43		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_19532277_c1_1120	3366	7138	126	41		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_19537812_c2_1293	3367	7139	150	49	39	0.0042

Description

pir: [LN:A70221] [AC:A70221] [PN:conserved hypothetical protein BBC08] [OR: *Borrelia burgdorferi*] [SR:, Lyme disease spirochete] [DB:pir2] >gp: [GI:g2689920] [LN:AE000791] [AC:AE000791] [PN:conserved hypothetical protein] [GN:BBC08] [OR: *Borrelia burgdorferi*] [SR:Lyme disease spirochete] [DB:genpept-bct2] [DE: *Borrelia burgdorferi* plasmid cp9, complete plasmid sequence.] [NT:similar to GB:U03641 PID:458212 percent identity:] [LE:5534] [RE:5980] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_19547783_f2_493	3368	7140	771	256	448	2.5e-42

Description

gp: [GI:g4481749] [LN:AF007865] [AC:AF007865] [PN: *BacR*] [GN: *bacR*] [OR: *Bacillus licheniformis*] [DB:genpept-bct2] [DE: *Bacillus licheniformis* bacitracin synthetase operon, complete sequence; *BacS* (*bacS*), *BcrA* (*bcrA*), *BcrB* (*bcrB*), and *BcrC* (*bcrC*) genes, complete cds.] [NT:44488] [LE:44497] [RE:45213] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_195885_f2_436	3369	7141	165	54		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_19589187_f3_689	3370	7142	207	68	57	0.019

Description

pir: [LN:F71027] [AC:F71027] [PN:hypothetical protein PH1514] [GN:PH1514] [OR: *Pyrococcus horikoshii*] [DB:pir2] >gp: [GI:d1031565:g3257939] [LN:AP000006] [AC:AP000006:AB005215:AB009510:AB009511:AB009512:AB009513:AB009514] [PN:310aa long hypothetical protein] [GN:PH1514] [OR: *Pyrococcus horikoshii*] [SR: *Pyrococcus horikoshii* (strain:OT3) DNA, clone: *Pyrococcus horikoshii*] [DB:genpept-bct1] [DE: *Pyrococcus horikoshii* OT3 genomic DNA, 1166001-1485000 nt. position(6/7).] [LE:183119] [RE:184051] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_19696951_c3_1486	3371	7143	183	60	193	2.6e-15

Description

pir: [LN:A70028] [AC:A70028] [PN:hypothetical protein yvAL] [GN:yvAL] [CL:protein-export protein secG] [OR: *Bacillus subtilis*] [DB:pir2] >gp: [GI:e1186051:g2635876] [LN:BSUB0018] [AC:Z99121:AL009126] [GN:yvAL] [FN:unknown] [OR: *Bacillus subtilis*] [DB:genpept-bct1] [DE: *Bacillus subtilis* complete genome (section 18 of 21): from 3399551 to 3609060.] [LE:54605] [RE:54835] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_19704062_f2_538	3372	7144	183	60		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_197127_c3_1411	3373	7145	132	43		

Description

NO-HIT

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_19714012_c1_939	3374	7146	144	47		

Description

NO-HIT

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_197152_c3_1343	3375	7147	348	115	257	4.3e-22

Description

gp: [GI:di1036083:g4001727] [LN:AB015981] [AC:AB015981] [PN:MnhC] [GN:mnhC]  
 [OR:Staphylococcus aureus] [SR:Staphylococcus aureus (strain:209P) DNA]  
 [DB:genpept-bct1] [DE:Staphylococcus aureus genes for OrfA, MnhA, MnhB, MnhC, MnhD,  
 MnhE, MnhF and MnhG, complete cds.] [LE:3642] [RE:3983] [DI:direct]

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_19726575_c1_942	3376	7148	144	47		

Description

NO-HIT

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_19765965_c1_1098	3377	7149	249	82	323	4.4e-29

Description

gp: [GI:g2226349] [LN:AF003593] [AC:AF003593] [PN:CspC] [GN:cspC] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:Staphylococcus aureus CspC (cspC) gene, complete cds.] [NT:similar to major cold-shock protein] [LE:444] [RE:644] [DI:direct]

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_19766886_f1_59	3378	7150	435	144	167	1.9e-12

Description

gp: [GI:e1294701:g3171734] [LN:BTPGI2XX] [AC:X13481] [OR:Bacillus thuringiensis] [DB:genpept-bct1] [DE:Bacillus thuringiensis plasmid pGI2 with transposon Tn4430.] [NT:ORF 2] [LE:6037] [RE:6849] [DI:direct]

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_19804502_f2_364	3379	7151	144	47		

Description

NO-HIT

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_19814387_c1_966	3380	7152	135	44		

Description

NO-HIT

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_19929556_f2_545	3381	7153	129	42		

Description

NO-HIT

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_2007677_f2_513	3382	7154	144	47		

Description

NO-HIT

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_2007767_c2_1199	3383	7155	126	41		

Description

NO-HIT

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_20110186_f3_688	3384	7156	153	50		

Description

NO-HIT

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_20322153_c2_1212	3385	7157	219	72		

Description

NO-HIT

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_20350875_c3_1515	3386	7158	123	40		

Description

NO-HIT

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_20485663_f2_563	3387	7159	210	69		

Description

NO-HIT

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_20491385_f1_252	3388	7160	144	47		

Description

NO-HIT

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_20604832_f3_692	3389	7161	558	185	106	0.0012

Description

gp: [GI:g552163] [LN:PFA10B] [AC:J03986] [OR:Plasmodium falciparum] [SR:P.falciparum (strain IMTM22) asexual erythrocytic form DNA, clon] [DB:genpept-inv1] [DE:P.falciparum 10b antigen gene, partial cds.] [NT:10b antigen] [LE:<1] [RE:>1124] [DI:direct]

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_20707877_c3_1457	3390	7162	123	40		

Description

NO-HIT

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_20734387_f3_640	3391	7163	159	52		

Description

NO-HIT

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_20830417_c3_1332	3392	7164	147	48		

Description

NO-HIT

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_20893828_c1_974	3393	7165	219	72		

Description

NO-HIT

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_20900017_c2_1239	3394	7166	2169	722	3396	0.0

Description

gp: [GI:e1393150:g4490609] [LN:SAU133495] [AC:AJ133495] [PN:ribonucleotide reductase major subunit] [GN:rir1] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:Staphylococcus aureus ribonucleotide reductase operon.] [LE:448] [RE:2604] [DI:direct]

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_209452_f1_276	3395	7167	648	215	754	9.4e-75

Description

gp: [GI:e255528:g1617429] [LN:SEABCTS] [AC:X99127] [PN:membrane protein] [FN:iron repressible ABC transport system] [OR:Staphylococcus epidermidis] [DB:genpept-bct1] [DE:S.epidermidis gene encoding ABC transport system.] [LE:878] [RE:1624] [DI:direct]

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_209627_c3_1444	3396	7168	1032	343	1571	2.5e-161

Description

gp: [GI:e1393151:g4490610] [LN:SAU133495] [AC:AJ133495] [PN:ribonucleotide reductase minor subunit] [GN:rir2] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:Staphylococcus aureus ribonucleotide reductase operon.] [LE:2722] [RE:3693] [DI:direct]

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_21490925_c1_1005	3397	7169	126	41		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_21509430_c1_962	3398	7170	132	43		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_21525061_c1_1016	3399	7171	681	226	110	0.00014

Description

sp: [LN:YB69\_HAEIN] [AC:P44118] [GN:HI1169] [OR:HAEMOPHILUS INFLUENZAE] [DE:HYPOTHETICAL PROTEIN HI1169] [SP:P44118] [DB:swissprot] >pir: [LN:A64021] [AC:A64021] [PN:hypothetical protein HI1169] [OR:Haemophilus influenzae] [DB:pir2] >gp: [GI:g1574096] [LN:U32797] [AC:U32797:L42023] [PN:H. influenzae predicted coding region HI1169] [GN:HI1169] [OR:Haemophilus influenzae Rd] [DB:genpept-bct2] [DE:Haemophilus influenzae Rd section 112 of 163 of the complete genome.] [NT:hypothetical protein; identified by GeneMark;] [LE:511] [RE:1077] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_21537811_c1_1007	3400	7172	1137	378	925	7.1e-93

Description

sp: [LN:CSBB\_BACSU] [AC:Q45539] [GN:CSBB] [OR:BACILLUS SUBTILIS] [DE:CSBB PROTEIN] [SP:Q45539] [DB:swissprot] >pir: [LN:JC5173] [AC:JC5173:G69607] [PN:stress response protein csbB] [GN:csbB] [CL:stress response protein csbB] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:g1387979] [LN:BACCSBB] [AC:L77099] [GN:csbB] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis csbB gene, complete cds.] [NT:similar to hypothetical protein from Synechocystis] [LE:310] [RE:1299] [DI:direct] >gp: [GI:e1182849:g2633183] [LN:BSUB0005] [AC:Z99108:AL009126] [PN:stress response protein] [GN:csbB] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 5 of 21): from 802821 to 1011250.] [NT:alternate gene name: yfhN] [SP:Q45539] [LE:127505] [RE:128494] [DI:direct] >gp: [GI:d1025396:g2804544] [LN:D85082] [AC:D85082] [PN:YfhN] [OR:Bacillus subtilis] [SR:Bacillus subtilis DNA] [DB:genpept-bct1] [DE:Bacillus subtilis DNA, genome sequence, 79 to 81 degree region.] [LE:20396] [RE:21385] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_21617215_f1_36	3401	7173	150	49		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_21726510_f2_612	3402	7174	126	41		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_21751287_f3_684	3403	7175	123	40		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_21883512_c3_1512	3404	7176	225	74		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_21897308_f2_541	3405	7177	261	86		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_21963877_c2_1273	3406	7178	123	40		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_22265936_c3_1452	3407	7179	1128	375	1557	7.6e-160

Description

pir: [LN:A55856] [AC:A55856] [PN:11m protein] [GN:11m] [CL:lipophilic protein 11m]  
[OR:Staphylococcus aureus] [DB:pir2] >gp: [GI:d1023388:g4433370] [LN:STASRM551A]  
[AC:D21131] [PN:lipophilic protein which affects bacterial lysis] [GN:11m]  
[OR:Staphylococcus aureus] [SR:Staphylococcus aureus (strain:SRM551) DNA,  
clone\_lib:lambda ZapII] [DB:genpept-bct1] [DE:Staphylococcus aureus gene for a  
participant in homogeneous expression of high-level methicillin resistance, complete  
cds.] [LE:148] [RE:1203] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_22381693_c3_1472	3408	7180	852	283	1187	1.2e-120

Description

sp: [LN:LGT\_STAAU] [AC:P52282] [GN:LGT] [OR:STAPHYLOCOCCUS AUREUS] [EC:2.4.99.-]  
[DE:PROLIPOPROTEIN DIACYLGLYCERYL TRANSFERASE,] [SP:P52282] [DB:swissprot]  
>gp: [GI:g1016770] [LN:SAU35773] [AC:U35773] [PN:prolipoprotein diacylglycerol  
transferase] [GN:lgt] [FN:transfer of diglyceride moiety to SH Group of]  
[OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:Staphylococcus aureus prolipoprotein  
diacylglycerol transferase(lgt) gene, complete cds.] [LE:297] [RE:1136] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_22391068_c1_1046	3409	7181	1056	351	1284	6.4e-131

Description

gp: [GI:e1330455:g3724158] [LN:SAA005352] [AC:AJ005352] [PN:lipoprotein] [GN:sstD]  
[FN:iron transporter] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:Staphylococcus  
aureus, Sst putative iron transport operon.] [LE:3066] [RE:4095] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_22446053_c2_1132	3410	7182	726	241	335	2.4e-30

Description

pir: [LN:A64479] [AC:A64479] [PN:DNA-(apurinic or apyrimidinic site) lyase, :endonuclease III] [CL:Methanococcus jannaschii conserved DNA-(apurinic or apyrimidinic site) lyase] [OR:Methanococcus jannaschii] [EC:4.2.99.18] [DB:pir2] [MP:FOR1403656-1404318] >gp: [GI:g1592082] [LN:U67584] [AC:U67584:L77117] [PN:endonuclease III, putative (nth2)] [GN:MJ1434] [OR:Methanococcus jannaschii] [DB:genpept-bct2] [DE:Methanococcus jannaschii section 126 of 150 of the complete genome.] [NT:similar to GB:U11289 SP:P39788 PID:533099] [LE:7078] [RE:7740] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_22462926_c1_1122	3411	7183	783	260	669	9.5e-66

Description

pir: [LN:H70023] [AC:H70023] [PN:N-acetyl-glucosamine catabolism homolog yutF] [GN:yutF] [CL:nagD protein] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1184308:g2635726] [LN:BSUB0017] [AC:Z99120:AL009126] [GN:yutF] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.] [NT:similar to N-acetyl-glucosamine catabolism] [LE:120087] [RE:120857] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_22687900_c3_1369	3412	7184	681	226	685	1.9e-67

Description

pir: [LN:G70000] [AC:G70000] [PN:two-component response regulator [YtsB] homolog ytsA] [GN:ytsA] [CL:ompR protein:response regulator homology] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1185913:g2635524] [LN:BSUB0016] [AC:Z99119:AL009126] [GN:ytsA] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.] [NT:similar to two-component response regulator [YtsB]] [LE:114498] [RE:115193] [DI:complement] >gp: [GI:g2293175] [LN:AF008220] [AC:AF008220] [PN:signal transduction regulator] [GN:ytsA] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis rrnB-dnaB genomic region.] [LE:65234] [RE:65929] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_22776938_c2_1323	3413	7185	156	51		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_22895400_f3_753	3414	7186	138	45		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_23437750_c1_938	3415	7187	171	56		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_23438461_c1_926	3416	7188	687	228	103	0.029

Description

gp: [GI:g5306158] [LN:AF160864] [AC:AF160864] [PN:orf1386] [GN:orf1386]  
 [OR:Mitochondrion Tetrahymena pyriformis] [SR:Tetrahymena pyriformis] [DB:genpept]  
 [DE:Tetrahymena pyriformis mitochondrial DNA, complete genome.] [NT:Open reading frame  
 ymf77 (CPGN); ATA initiation] [LE:22317] [RE:26477] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_23439005_f1_6	3417	7189	141	46		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_23439061_c1_984	3418	7190	531	176	258	3.4e-22

Description

pir: [LN:F69927] [AC:F69927] [PN:hypothetical protein yosT] [GN:yosT] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1185472:g2634393] [LN:BSUB0011] [AC:Z99114:AL009126] [GN:yosT] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 11 of 21): from 2000171 to 2207900.] [LE:157797] [RE:158246] [DI:complement] >gp: [GI:g3025644] [LN:AF020713] [AC:AF020713] [PN:unknown] [GN:yosT] [OR:Bacteriophage SPBc2] [DB:genpept-phg] [DE:Bacteriophage SPBc2 complete genome.] [LE:127274] [RE:127723] [DI:direct] >gp: [GI:g2522410] [LN:AF012906] [AC:AF012906:U80600] [PN:unknown] [GN:yojV] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis yojP gene, partial cds; yojQ/S, yojR, yojT, yojU, yojV, yojW, yojX, yojY, yojZ, and yokA genes, complete cds.] [LE:4921] [RE:5370] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_23444838_c2_1267	3419	7191	264	87	373	2.2e-34

Description

gp: [GI:e1387399:g4379428] [LN:SAAJ3781] [AC:AJ223781] [PN:thioredoxin reductase] [GN:trxR] [OR:Staphylococcus aureus] [DB:genpept-bct1] [EC:1.6.4.5] [DE:Staphylococcus aureus trxR gene.] [LE:1262] [RE:2197] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_23445175_f3_674	3420	7192	135	44		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_23445890_c2_1177	3421	7193	492	163	333	3.8e-30

Description

pir: [LN:S74709] [AC:S74709] [PN:hypothetical protein sll1188] [OR:Synechocystis sp.] [SR:PCC 6803, , PCC 6803] [SR:PCC 6803, ] [DB:pir2] >gp: [GI:d1017593:g1651934] [LN:D90901] [AC:D90901:AB001339] [PN:hypothetical protein] [OR:Synechocystis sp.] [SR:Synechocystis sp. (strain:PCC6803) DNA] [DB:genpept-bct1] [DE:Synechocystis sp. PCC6803 complete genome, 3/27, 271600-402289.] [NT:ORF\_ID:sll1188] [LE:42106] [RE:42600] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503001001_23446912_f2_597	3422	7194	123	40		
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Description

NO-HIT

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503001001_2345062_f3_639	3423	7195	171	56		
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Description

NO-HIT

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503001001_23450_c3_1490	3424	7196	189	62		
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Description

NO-HIT

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503001001_23469552_c1_923	3425	7197	207	68		
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Description

NO-HIT

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503001001_23475892_c1_1121	3426	7198	1362	453	707	9.0e-70
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Description

pir:[LN:G70015] [AC:G70015] [PN:conserved hypothetical protein yunD] [GN:yunD]  
[OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1184316:g2635734] [LN:BSUB0017]  
[AC:Z99120:AL009126] [GN:yunD] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1]  
[DE:Bacillus subtilis complete genome (section 17 of 21): from 3197001 to 3414420.]  
[NT:similar to hypothetical proteins] [LE:125728] [RE:127116] [DI:complement]

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_23476517_c2_1259	3427	7199	1296	431	638	1.8e-62

Description

sp:[LN:CMF1\_BACSU] [AC:P39145] [GN:COMFA:COMF1] [OR:BACILLUS SUBTILIS] [DE:COMF OPERON PROTEIN 1] [SP:P39145] [DB:swissprot] >pir:[LN:G69602] [AC:G69602:S77620:S35011:I40387:S28597] [PN:late competence protein required for DNA uptake comFA:ATP-dependent DNA helicase/translocase comF1] [GN:comFA:comF1] [CL:DEAD/H box helicase homology] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:g580841] [LN:BSCOMFG] [AC:Z18629] [PN:F1] [GN:comForf1] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis comF gene.] [SP:P39145] [LE:952] [RE:2343] [DI:direct] >gp:[GI:e1184453:g2636073] [LN:BSUB0019] [AC:Z99122:AL009126] [PN:late competence protein] [GN:comFA] [FN:required for DNA uptake (competence)] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091 to 3809700.] [SP:P39145] [LE:44137] [RE:45528] [DI:complement] >gp:[GI:g1762332] [LN:BSU56901] [AC:U56901] [GN:comFA] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis putative transcriptional regulator (yvhJ), Ycr59c/YigZ homolog (yvhK), histidine kinase (degS), transcriptional regulator of degradation enzyme (degU), (degV), (comFA), (comFB), (comFC), flagellar protein (yviB), negative regulator of flagellin(flgM), flagellar protein (yviC), flagellar-hook associated protein1 (flgK), flagellar-hook associated protein 3 (flgL), (yviE), transmembrane protein (yviF), (csrA), flagellin (hag), flagellar protein (yviH), flagellar hook-associated protein 2 (fliD), flagellar protein (fliS), flagellar protein (fliT), sigma-54 modulator homolog (yviI), and (secA) genes, complete cds.] [NT:involved in transformation] [LE:5065] [RE:6456] [DI:direct] >gp:[GI:e1184453:g2636073] [LN:BSUB0019] [AC:Z99122:AL009126] [PN:late competence protein] [GN:comFA] [FN:required for DNA uptake (competence)] [OR:Bacillus subtilis] [DB:genpept] [DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091 to 3809700.] [SP:P39145] [LE:44137] [RE:45528] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_23492127_f2_368	3428	7200	453	150		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_23494051_f2_444	3429	7201	1101	366	336	1.8e-30

Description

sp:[LN:YHCK\_BACSU] [AC:P54595] [GN:YHCK] [OR:BACILLUS SUBTILIS] [DE:HYPOTHETICAL 40.7 KD PROTEIN IN CSPB-GLPP INTERGENIC REGION] [SP:P54595] [DB:swissprot] >pir:[LN:G69822] [AC:G69822] [PN:conserved hypothetical protein yhck] [GN:yhcK] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e233892:g1239987] [LN:BS75DGREG] [AC:X96983] [PN:hypothetical protein] [GN:yhcK] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis chromosomal DNA (region 75 degrees: cspB upstream of glpPFKD operon).] [NT:similarity to hypothetical proteins from] [SP:P54595] [LE:6616] [RE:7695] [DI:complement] >gp:[GI:e1182901:g2633235] [LN:BSUB0005] [AC:Z99108:AL009126] [GN:yhcK] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 5 of 21): from 802821 to 1011250.] [NT:similar to hypothetical proteins] [SP:P54595] [LE:182422] [RE:183501] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_235042_c1_1064	3430	7202	141	46		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_2352140_f3_902	3431	7203	156	51		

Description

NO-HIT

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_23523326_c3_1385	3432	7204	1242	413	416	6.1e-39

Description

sp: [LN:YICK\_ECOLI] [AC:P31436] [GN:YICK] [OR:ESCHERICHIA COLI] [DE:HYPOTHETICAL 43.5 KD PROTEIN IN SELC-NLPA INTERGENIC REGION] [SP:P31436] [DB:swissprot] >pir: [LN:D65167] [AC:D65167] [PN:probable membrane protein yick] [GN:yick] [OR:Escherichia coli] [DB:pir2] >gp: [GI:g290508] [LN:ECOUW82] [AC:L10328] [GN:o394] [FN:unknown] [OR:Escherichia coli] [SR:Escherichia coli K12 strain MG1655; lambda clones EC14-52] [DB:genpept-bct1] [DE:E. coli; the region from 81.5 to 84.5 minutes.] [NT:similar to unidentified ORF near 47 minutes] [LE:26345] [RE:27529] [DI:direct] >gp: [GI:g1790091] [LN:AE000443] [AC:AE000443:U00096] [PN:two-module transport protein] [GN:yick] [FN:putative transport; Not classified] [OR:Escherichia coli] [DB:genpept-bct2] [DE:Escherichia coli K-12 MG1655 section 333 of 400 of the completestgenome.] [NT:o394; 100 pct identical to YICK\_ECOLI SW:] [LE:8286] [RE:9470] [DI:direct]

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_23572177_c3_1482	3433	7205	1194	397	1792	9.5e-185

Description

gp: [GI:e1393155:g4490614] [LN:SAU133520] [AC:AJ133520] [PN:phosphoglycerate kinase] [GN:pgk] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:Staphylococcus aureus gap operon (gapR, gap, pgk and tpi genes).] [LE:2995] [RE:4185] [DI:direct]

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_23600175_f2_616	3434	7206	123	40		

Description

NO-HIT

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_23617338_f1_66	3435	7207	528	175	215	1.2e-24

Description

sp: [LN:YAGU\_ECOLI] [AC:P77262] [GN:YAGU] [OR:ESCHERICHIA COLI] [DE:HYPOTHETICAL 23.0 KD PROTEIN IN INTF-EAEH INTERGENIC REGION] [SP:P77262] [DB:swissprot] >pir: [LN:G64754] [AC:G64754] [PN:probable membrane protein yagU] [GN:yagU] [OR:Escherichia coli] [DB:pir2] >gp: [GI:g1657488] [LN:ECU73857] [AC:U73857] [OR:Escherichia coli] [DB:genpept-bct1] [DE:Escherichia coli chromosome minutes 6-8.] [NT:hypothetical protein] [LE:10789] [RE:11403] [DI:direct] >gp: [GI:g1786481] [LN:AE000136] [AC:AE000136:U00096] [PN:orf, hypothetical protein] [GN:yagU] [FN:orf; Unknown] [OR:Escherichia coli] [DB:genpept-bct2] [DE:Escherichia coli K-12 MG1655 section 26 of 400 of the completestgenome.] [NT:o204; 26 pct identical to 46 residues of approx.] [LE:7372] [RE:7986] [DI:direct]

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503001001_23621010_c1_971	3436	7208	843	280	167	1.5e-10
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Description

pir:[LN:E69777] [AC:E69777] [PN:transcription regulator AraC/XylS family homolog ydeC] [GN:ydeC] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:d1020103:g1881323] [LN:AB001488] [AC:AB001488] [GN:ydeC] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:168) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis genome sequence, 148 kb sequence of the region between 35 and 47 degree.] [NT:PROBABLE HTH\_ARAC\_FAMILY OF TRANSCRIPTIONAL] [LE:94733] [RE:95608] [DI:complement] >gp:[GI:e1182481:g2632815] [LN:BSUB0003] [AC:Z99106:AL009126] [GN:ydeC] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 3 of 21): from 402751 to 611850.] [NT:similar to transcriptional regulator (AraC/XylS] [LE:158478] [RE:159353] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503001001_23626000_f2_582	3437	7209	168	55		
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503001001_23629040_c2_1318	3438	7210	132	43		
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503001001_23631928_f2_520	3439	7211	228	75		
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503001001_23634651_c1_964	3440	7212	1044	347	549	5.0e-53
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Description

pir:[LN:H70000] [AC:H70000] [PN:two-component sensor histidine kinase homolog ytsB] [GN:ytsB] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1185912:g2635523] [LN:BSUB0016] [AC:Z99119:AL009126] [GN:ytsB] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 16 of 21): from 2997771 to 3213410.] [NT:similar to two-component sensor histidine kinase] [LE:113501] [RE:114505] [DI:complement] >gp:[GI:g2293176] [LN:AF008220] [AC:AF008220] [PN:signal transduction protein kinase] [GN:ytsB] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis rrnB-dnaB genomic region.] [LE:65922] [RE:66926] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503001001_23672137_c2_1196	3441	7213	957	318	260	6.6e-32
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Description

pir:[LN:S76964] [AC:S76964] [PN:hypothetical protein] [OR:Synechocystis sp.] [SR:PCC 6803, PCC 6803] [SR:PCC 6803,] [DB:pir2] >gp:[GI:d1019609:g1653966] [LN:D90917] [AC:D90917:AB001339] [PN:47 kD protein] [OR:Synechocystis sp.] [SR:Synechocystis sp. (strain:PCC6803) DNA] [DB:genpept-bct1] [DE:Synechocystis sp. PCC6803 complete genome, 27/27, 3418852-3573470.] [NT:ORF\_ID:slr0609] [LE:151573] [RE:152724] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503001001_23672562_c1_924	3442	7214	297	98	86	0.0034
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Description

gp: [GI:e8900:g1335718] [LN:PFRESAR1] [AC:X05182] [PN:ring-infected erythrocyte surface antigen] [GN:RESA] [OR:Plasmodium falciparum] [SR:malaria parasite P. falciparum] [DB:genpept-inv1] [DE:P.falciparum FC27 Ag46 RESA mRNA for ring-infected erythrocytesurface antigen.] [SP:P13830] [LE:<1] [RE:>955] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503001001_23703750_c1_1095	3443	7215	639	212		
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503001001_23728412_c3_1509	3444	7216	699	232	726	8.7e-72
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Description

pir: [LN:C70020] [AC:C70020.] [PN:conserved hypothetical protein yusB] [GN:yusB] [CL:probable transport protein yaeE] [OR:Bacillus subtilis] [DB:pir2]  
 >gp: [GI:e1184352:g2635770] [LN:BSUB0017] [AC:Z99120:AL009126] [GN:yusB] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 17 of 21): from 3197001 to 3414420.] [NT:similar to hypothetical proteins] [LE:164664] [RE:165332] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503001001_23844575_c2_1274	3445	7217	1062	353	1442	1.2e-147
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Description

gp: [GI:e1393153:g4490612] [LN:SAU133520] [AC:AJ133520] [PN:gap regulator] [GN:gapR] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:Staphylococcus aureus gap operon (gapR, gap, pgk and tpi genes).] [LE:779] [RE:1792] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503001001_23984775_f1_83	3446	7218	153	50		
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503001001_23989061_f2_399	3447	7219	138	45		
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503001001_2401430_c3_1473	3448	7220	762	253	1076	7.1e-109
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Description

gp: [GI:e1387399:g4379428] [LN:SAAJ3781] [AC:AJ223781] [PN:thioredoxin reductase] [GN:trxB] [OR:Staphylococcus aureus] [DB:genpept-bct1] [EC:1.6.4.5] [DE:Staphylococcus aureus trxB gene.] [LE:1262] [RE:2197] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_24022582_f2_316	3449	7221	150	49		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_24033567_c2_1316	3450	7222	450	149	207	8.6e-17

Description

pir: [LN:G70023] [AC:G70023] [PN:hypothetical protein yutE] [GN:yutE] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1184309:g2635727] [LN:BSUB0017] [AC:Z99120:AL009126] [GN:yutE] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 17 of 21): from 3197001 to 3414420.] [LE:120886] [RE:121320] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_24218785_c2_1275	3451	7223	1047	348	1597	4.4e-164

Description

gp: [GI:e1393154:g4490613] [LN:SAU133520] [AC:AJ133520] [PN:glyceraldehyde-3-phosphate dehydrogenase] [GN:gap] [FN:transferrin binding protein] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:Staphylococcus aureus gap operon (gapR, gap, pgk and tpi genes).] [NT:putative] [LE:1845] [RE:2855] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_24230001_f2_362	3452	7224	258	85		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_24240888_f1_281	3453	7225	129	42		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_24242285_c3_1516	3454	7226	1056	351	439	2.2e-41

Description

gp: [GI:g4981378] [LN:AE001751] [AC:AE001751:AE000512] [PN:hemolysin-related protein] [GN:TM0845] [OR:Thermotoga maritima] [DB:genpept-bct2] [DE:Thermotoga maritima section 63 of 136 of the complete genome.] [NT:similar to GB:AE000783 percent identity: 61.61;] [LE:5310] [RE:6677] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_24251500_f2_416	3455	7227	135	44		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_24253153_f1_150	3456	7228	129	42		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_24256287_c2_1260	3457	7229	141	46		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_24258388_c3_1405	3458	7230	1507	168	102	0.0053

Description

gp: [GI:e1407794:g4493938] [LN:PFMAL3P5] [AC:AL034556] [GN:MAL3P5.10] [OR:Plasmodium falciparum] [SR:malaria parasite P. falciparum] [DB:genpept-inv1] [DE:Plasmodium falciparum MAL3P5, complete sequence.] [NT:predicted using hexExon; MAL3P5.10 (PFC0620w),] [LE:46925] [RE:48919] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_24259762_f3_679	3459	7231	132	43		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_24266888_c3_1413	3460	7232	123	40		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_24272125_c2_1292	3461	7233	261	86	72	0.024

Description

gp: [GI:g942589] [LN:MIU29676] [AC:U29676:X55271] [PN:unknown] [OR:Mycoplasma iowae] [DB:genpept-bct2] [DE:Mycoplasma iowae 16S rRNA gene, complete sequence, and 23S rRNA gene, partial sequence.] [LE:<1] [RE:438] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_24297000_f2_548	3462	7234	225	74		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_24329053_c1_979	3463	7235	444	147	142	2.8e-09

Description

gp: [GI:g3329623] [LN:CELF36H12] [AC:AF078790] [GN:F36H12.3] [OR:Caenorhabditis elegans] [DB:genpept-inv2] [DE:Caenorhabditis elegans cosmid F36H12.] [NT:coded for by C. elegans cDNA CEMSF30F] [LE:21606:21872:22500:22677] [RE:21701:22454:22629:22875] [DI:directJoin]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_24335801_c2_1326	3464	7236	138	45		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_24345257_f3_652	3465	7237	168	55		

Description

NO-HIT

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_24347175_c3_1416	3466	7238	165	54		

Description

NO-HIT

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_24391937_c1_1068	3467	7239	759	252	105	0.0062

Description

pir:[LN:E70031] [AC:E70031] [PN:hypothetical protein yvcD] [GN:yvcD]  
 [CL:tetratricopeptide repeat homology] [OR:Bacillus subtilis] [DB:pir2]  
 >gp:[GI:e1186169:g2635994] [LN:BSUB0018] [AC:Z99121:AL009126] [GN:yvcD] [FN:unknown]  
 [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section  
 18 of 21): from 3399551to 3609060.] [LE:175675] [RE:177129] [DI:complement]  
 >gp:[GI:e313021:g1945645] [LN:BSZ94043] [AC:Z94043] [PN:hypothetical protein] [GN:yvcD]  
 [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis genomic DNA fragment (88 kb).]  
 [LE:4542] [RE:5996] [DI:direct]

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_24397952_c1_1067	3468	7240	681	226	119	0.00011

Description

pir:[LN:E70031] [AC:E70031] [PN:hypothetical protein yvcD] [GN:yvcD]  
 [CL:tetratricopeptide repeat homology] [OR:Bacillus subtilis] [DB:pir2]  
 >gp:[GI:e1186169:g2635994] [LN:BSUB0018] [AC:Z99121:AL009126] [GN:yvcD] [FN:unknown]  
 [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section  
 18 of 21): from 3399551to 3609060.] [LE:175675] [RE:177129] [DI:complement]  
 >gp:[GI:e313021:g1945645] [LN:BSZ94043] [AC:Z94043] [PN:hypothetical protein] [GN:yvcD]  
 [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis genomic DNA fragment (88 kb).]  
 [LE:4542] [RE:5996] [DI:direct]

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_24406577_c3_1415	3469	7241	390	129		

Description

NO-HIT

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_24407637_f1_57	3470	7242	243	80		

Description

NO-HIT

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_24415930_f2_310	3471	7243	1068	355	977	2.2e-98

Description

pir: [LN:D70024] [AC:D70024] [PN:NADH dehydrogenase homolog yutJ] [GN:yutJ] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1184299:g2635717] [LN:BSUB0017] [AC:Z99120:AL009126] [GN:yutJ] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 17 of 21): from 3197001 to 3414420.] [NT:similar to NADH dehydrogenase] [LE:110924] [RE:111916] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_24429650_c3_1408	3472	7244	1197	398	848	1.0e-84

Description

sp: [LN:NAGA\_BACSU] [AC:O34450] [GN:NAGA] [OR:BACILLUS SUBTILIS] [EC:3.5.1.25] [DE:DEACETYLASE] [SP:O34450] [DB:swissprot] >pir: [LN:A69664] [AC:A69664] [PN:N-acetylglucosamine-6-phosphate deacetylase nagA] [GN:nagA] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1186189:g2636014] [LN:BSUB0018] [AC:Z99121:AL009126] [PN:N-acetylglucosamine-6-phosphate deacetylase] [GN:nagA] [FN:N-acetyl glucosamine utilization] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:3.5.1.25] [DE:Bacillus subtilis complete genome (section 18 of 21): from 3399551 to 3609060.] [SP:O34450] [LE:194866] [RE:196056] [DI:direct] >gp: [GI:g2618856] [LN:AF017113] [AC:AF017113] [PN:N-acetylglucosamine 6-P deacetylase] [GN:nagA] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis 300-304 degree genomic sequence.] [LE:31777] [RE:32967] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_24479842_c1_1106	3473	7245	558	185	256	5.5e-22

Description

pir: [LN:D69800] [AC:D69800] [PN:conserved hypothetical protein yfhC] [GN:yfhC] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1182838:g2633172] [LN:BSUB0005] [AC:Z99108:AL009126] [GN:yfhC] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 5 of 21): from 802821 to 1011250.] [NT:similar to hypothetical proteins] [LE:120274] [RE:120858] [DI:direct] >gp: [GI:d1025385:g2804533] [LN:D85082] [AC:D85082] [PN:YfhC] [OR:Bacillus subtilis] [SR:Bacillus subtilis DNA] [DB:genpept-bct1] [DE:Bacillus subtilis DNA, genome sequence, 79 to 81 degree region.] [LE:13165] [RE:13749] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_24490676_c2_1179	3474	7246	141	46		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_24506712_c2_1240	3475	7247	975	324	879	5.3e-88

Description

gp: [GI:e1330453:g3724156] [LN:SAA005352] [AC:AJ005352] [PN:membrane protein] [GN:sstB] [FN:iron transport] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:Staphylococcus aureus, Sst putative iron transport operon.] [LE:1451] [RE:2132] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503001001_24507932_c1_1027	3476	7248	600	199	322	5.6e-29
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Description

pir: [LN:D69924] [AC:D69924] [PN:hypothetical protein yorS] [GN:yorS] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1185499:g2634420] [LN:BSUB0011] [AC:Z99114:AL009126] [GN:yorS] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 11 of 21): from 2000171 to 2207900.] [LE:172005] [RE:172523] [DI:complement] >gp: [GI:g3025618] [LN:AF020713] [AC:AF020713] [PN:unknown] [GN:yorS] [OR:Bacteriophage SPBc2] [DB:genpept-phg] [DE:Bacteriophage SPBc2 complete genome.] [LE:112997] [RE:113515] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503001001_24611512_c2_1139	3477	7249	129	42		
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503001001_24616050_f2_445	3478	7250	150	49		
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503001001_24640828_c2_1138	3479	7251	516	171		
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503001001_24642632_f3_765	3480	7252	1245	414	1245	8.7e-127
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Description

sp: [LN:PEPT\_BACSU] [AC:P55179] [GN:PEPT] [OR:BACILLUS SUBTILIS] [EC:3.4.11.-] [DE:PEPTIDASE T, (AMINOTRIPEPTIDASE) (TRIPEPTIDASE)] [SP:P55179] [DB:swissprot] >pir: [LN:H69674] [AC:H69674] [PN:aminotripeptidase, peptidase T] [GN:pepT] [OR:Bacillus subtilis] [EC:3.4.11.-] [DB:pir2] >gp: [GI:e254163:g1429259] [LN:BSGALE] [AC:X99339] [GN:pepT] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B. subtilis orfs 1,2,3,4, pepT and gale genes.] [SP:P55179] [LE:5267] [RE:6499] [DI:direct] >gp: [GI:e1186391:g2636427] [LN:BSUB0020] [AC:Z99123:AL009126] [PN:peptidase T (tripeptidase)] [GN:pepT] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:3.4.11.-] [DE:Bacillus subtilis complete genome (section 20 of 21): from 3798401 to 4010550.] [SP:P55179] [LE:195467] [RE:196699] [DI:direct] >gp: [GI:d1012379:g1783235] [LN:D83026] [AC:D83026:D45911] [GN:pepT] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:BGSC 1A1) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis genome sequence covering lic-cel region.] [NT:highly homologous to tripeptidases (peptidase T)] [LE:27766] [RE:28998] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_24650427_f2_349	3481	7253	330	109	331	6.2e-30

Description

pir:[LN:C69772] [AC:C69772] [PN:thioredoxin homolog ydbP] [GN:ydbP]  
 [CL:thioredoxin:thioredoxin homology] [OR:Bacillus subtilis] [DB:pir2]  
 >gp:[GI:d1020045:g1881265] [LN:AB001488] [AC:AB001488] [GN:ydbP] [OR:Bacillus subtilis]  
 [SR:Bacillus subtilis (strain:168) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis genome  
 sequence, 148 kb sequence of the region between 35 and 47 degree.] [NT:PROBABLE  
 THIOREDOXIN.] [LE:40816] [RE:41136] [DI:complement] >gp:[GI:e1182421:g2632755]  
 [LN:BSUB0003] [AC:Z99106:AL009126] [GN:ydbP] [FN:unknown] [OR:Bacillus subtilis]  
 [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 3 of 21): from 402751  
 to 611850.] [NT:similar to thioredoxin] [LE:104560] [RE:104880] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_24650462_c1_944	3482	7254	1515	504	848	1.0e-84

Description

pir:[LN:G70008] [AC:G70008] [PN:NADH dehydrogenase (ubiquinone) homolog yufD] [GN:yufD]  
 [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1184241:g2635659] [LN:BSUB0017]  
 [AC:Z99120:AL009126] [GN:yufD] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1]  
 [DE:Bacillus subtilis complete genome (section 17 of 21): from 3197001 to 3414420.]  
 [NT:similar to NADH dehydrogenase (ubiquinone)] [LE:51840] [RE:53282] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_24664840_c2_1203	3483	7255	1968	655	1694	2.3e-174

Description

pir:[LN:H69626] [AC:H69626] [PN:PTS fructose-specific enzyme IIBC component fruA]  
 [GN:fruA] [CL:phosphotransferase system enzyme II,  
 fructose-specific:phosphotransferase system mannitol-specific enzyme II factor III  
 homology] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1185030:g2633811] [LN:BSUB0008]  
 [AC:Z99111:AL009126] [PN:phosphotransferase system (PTS)] [GN:fruA] [OR:Bacillus  
 subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 8 of 21):  
 from 1394791 to 1603020.] [LE:113871] [RE:115778] [DI:direct] >gp:[GI:g3282125]  
 [LN:AF012285] [AC:AF012285:AF012284:U51911] [PN:fructose PTS IIABC] [GN:fruA]  
 [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis mobA-nprE gene region.]  
 [NT:similar to fructose-specific PTS system IIBC] [LE:14359] [RE:16266] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_24796927_f1_61	3484	7256	789	262	325	2.7e-29

Description

pir:[LN:E69883] [AC:E69883] [PN:phage-related replication protein homolog ymaC]  
 [GN:ymaC] [CL:phage-related replication protein] [OR:Bacillus subtilis] [DB:pir2]  
 >gp:[GI:e1183386:g2634111] [LN:BSUB0010] [AC:Z99113:AL009126] [GN:ymaC] [FN:unknown]  
 [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section  
 10 of 21): from 1781201 to 2014980.] [NT:similar to phage-related protein] [LE:81490]  
 [RE:82197] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_24803125_c1_993	3485	7257	978	325	982	6.5e-99

Description

sp: [LN:MDH\_BACIS] [AC:Q59202] [GN:MDH] [OR:BACILLUS ISRAELI] [EC:1.1.1.37] [DE:MALATE DEHYDROGENASE,] [SP:Q59202] [DB:swissprot] >pir:[LN:S61213] [AC:S61213] [PN:malate dehydrogenase,] [CL:L-lactate dehydrogenase] [OR:Bacillus israeli] [EC:1.1.1.37] [DB:pir2] >gp:[GI:g963019] [LN:BIDNAMD] [AC:X90527] [PN:malate dehydrogenase] [OR:Bacillus israeli] [DB:genpept-bct1] [EC:1.1.1.37] [DE:B.israeli DNA for malate dehydrogenase gene.] [SP:Q59202] [LE:291] [RE:1229] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_24803332_c2_1305	3486	7258	840	279	712	2.6e-70

Description

pir:[LN:B70020] [AC:B70020] [PN:conserved hypothetical protein yusA] [GN:yusA] [CL:lipoprotein-28] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1184351:g2635769] [LN:BSUB0017] [AC:Z99120:AL009126] [GN:yusA] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.] [NT:similar to hypothetical proteins] [LE:163826] [RE:164650] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_2531500_c3_1360	3487	7259	177	58		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_25401377_c1_1045	3488	7260	852	283	939	2.3e-94

Description

gp:[GI:e1330454:g3724157] [LN:SAA005352] [AC:AJ005352] [PN:ATP binding protein] [GN:SstC] [FN:iron transport] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:Staphylococcus aureus, Sst putative iron transport operon.] [LE:2186] [RE:2947] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_25401675_c2_1319	3489	7261	174	57		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_25415802_c1_1102	3490	7262	126	41		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_25473782_c3_1498	3491	7263	186	61		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_25492312_f1_302	3492	7264	126	41		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_25572180_c1_956	3493	7265	1272	423	895	1.1e-89

Description

sp: [LN:YXJA\_BACSU] [AC:P42312] [GN:YXJA:N15HR] [OR:BACILLUS SUBTILIS] [DE:HYPOTHETICAL 43.7 KD PROTEIN IN KATB 3'REGION] [SP:P42312] [DB:swissprot] >pir: [LN:G70078] [AC:G70078] [PN:pyrimidine nucleoside transport homolog yxjA] [GN:yxjA] [CL:pyrimidine nucleoside transport protein nupC] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1186401:g2636437] [LN:BSUB0020] [AC:Z99123:AL009126] [GN:yxjA] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.] [NT:similar to pyrimidine nucleoside transport] [SP:P42312] [LE:206141] [RE:207334] [DI:direct] >gp: [GI:e1184627:g2636448] [LN:BSUB0021] [AC:Z99124:AL009126] [GN:yxjA] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.] [NT:similar to pyrimidine nucleoside transport] [SP:P42312] [LE:5261] [RE:6454] [DI:direct] >gp: [GI:d1012369:g665999] [LN:D83026] [AC:D83026:D45911] [GN:yxjA] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:BGSC 1A1) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis genome sequence covering lic-cel region.] [NT:homologous to pyrimidine nucleoside transport] [LE:17131] [RE:18324] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_25585891_c2_1218	3494	7266	1980	659	1949	2.2e-201

Description

pir: [LN:D69815] [AC:D69815] [PN:conserved hypothetical protein yfnI] [GN:yfnI] [CL:Bacillus subtilis probable anion-binding protein yf1E] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1182705:g2633039] [LN:BSUB0004] [AC:Z99107:AL009126] [GN:yfnI] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 4 of 21): from 600701 to 813890.] [NT:alternate gene name: yetP; similar to hypothetical] [LE:195080] [RE:197041] [DI:direct] >gp: [GI:d1020933:g2116767] [LN:D86418] [AC:D86418] [PN:YfnI] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:AC327) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis genomic DNA 69-70 degree region, partialsequence.] [LE:16150] [RE:18111] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_25806300_f1_275	3495	7267	750	249	1270	2.0e-129

Description

gp: [GI:e255626:g1617428] [LN:SEABCTS] [AC:X99127] [PN:ATP binding protein] [FN:iron repressible ABC transport system] [OR:Staphylococcus epidermidis] [DB:genpept-bct1] [DE:S.epidermidis gene encoding ABC transport system.] [LE:41] [RE:787] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_26171927_c2_1246	3496	7268	342	113	221	2.8e-18

Description

sp: [LN:YTXJ\_BACSU] [AC:P39914] [GN:YTXJ] [OR:BACILLUS SUBTILIS] [DE:(ORF3)] [SP:P39914] [DB:swissprot] >pir: [LN:S21420] [AC:S21420:F70003:S71003] [PN:general stress protein homolog ytxJ] [GN:ytxJ] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:g39815] [LN:BSAROAG] [AC:X65945] [GN:orf 2] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis aroA-aroG gene.] [SP:P39914] [LE:105] [RE:431] [DI:direct] >gp: [GI:e1185849:g2635460] [LN:BSUB0016] [AC:Z99119:AL009126] [GN:ytxJ] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.] [NT:alternate gene name: csb40; similar to general] [SP:P39914] [LE:48061] [RE:48387] [DI:complement] >gp: [GI:g2293219] [LN:AF008220] [AC:AF008220] [PN:YtxJ] [GN:ytxJ] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis rrnB-dnaB genomic region.] [LE:132039] [RE:132365] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_26176693_f2_482	3497	7269	828	275	685	1.9e-67

Description

pir: [LN:A69162] [AC:A69162] [PN:gufA protein homolog MTH473] [GN:MTH473] [CL:gufA protein] [OR:Methanobacterium thermoautotrophicum] [DB:pir2] >gp: [GI:g2621542] [LN:AE000831] [AC:AE000831:AE000666] [PN:conserved protein] [GN:MTH473] [OR:Methanobacterium thermoautotrophicum] [DB:genpept-bct1] [DE:Methanobacterium thermoautotrophicum from bases 404817 to 415582(section 37 of 148) of the complete genome.] [NT:Function Code:14.01 - Unknown, Conserved protein;] [LE:9769] [RE:10548] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_2618827_c1_1042	3498	7270	288	95	75	0.023

Description

sp: [LN:LUXY\_VIBFI] [AC:P21578] [GN:LUXY] [OR:VIBRIO FISCHERI] [DE:YELLOW FLUORESCENT PROTEIN (YFP)] [SP:P21578] [DB:swissprot] >pir: [LN:A36037] [AC:A36037:A39946] [PN:yellow fluorescent protein:luxY protein] [GN:luxY] [CL:riboflavin synthase alpha chain] [OR:Vibrio fischeri] [DB:pir2] >gp: [GI:g155235] [LN:VIBLUXY] [AC:M60852] [PN:yellow fluorescent protein] [GN:luxY] [OR:Vibrio fischeri] [SR:V.fischeri (strain Y-1) DNA] [DB:genpept-bct1] [DE:Vibrio fischeri yellow fluorescent protein (luxY) gene, completecds.] [LE:45] [RE:629] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_26190785_c2_1306	3499	7271	1287	428	1408	4.7e-144

Description

pir: [LN:F70019] [AC:F70019] [PN:NifS protein homolog homolog yurW] [GN:yurW] [CL:nifs protein] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1184347:g2635765] [LN:BSUB0017] [AC:Z99120:AL009126] [GN:yurW] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.] [NT:similar to NifS protein homolog] [LE:159503] [RE:160723] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_26204837_f1_69	3500	7272	159	52		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_26211552_c2_1270	3501	7273	984	327	1034	2.0e-104

Description

pir: [LN:B70032] [AC:B70032] [PN:conserved hypothetical protein yvcL] [GN:yvcL] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1186163:g2635988] [LN:BSUB0018] [AC:Z99121:AL009126] [GN:yvcL] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 18 of 21): from 3399551 to 3609060.] [NT:similar to hypothetical proteins] [LE:169083] [RE:170033] [DI:complement] >gp: [GI:e313028:g1945652] [LN:BSZ94043] [AC:Z94043] [PN:hypothetical protein] [GN:yvcL] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B. subtilis genomic DNA fragment (88 kb).] [NT:similar to Y103\_MYCGE hypothetical protein mg103] [LE:11638] [RE:12588] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_26259638_f1_134	3502	7274	765	254	176	2.2e-11

Description

pir: [LN:B70798] [AC:B70798] [PN:probable membrane protein] [GN:Rv3737] [OR:Mycobacterium tuberculosis] [DB:pir2] >gp: [GI:e1264597:g2960161] [LN:MTV025] [AC:AL022121:AL123456] [PN:hypothetical protein Rv3737] [GN:Rv3737] [OR:Mycobacterium tuberculosis] [DB:genpept-bct1] [DE:Mycobacterium tuberculosis H37Rv complete genome; segment 155/162.] [NT:Rv3737, (MTV025.085), len: 529. Probable membrane] [LE:94796] [RE:96385] [DI:direct] >gp: [GI:e1264597:g2960161] [LN:MTV025] [AC:AL022121:AL123456] [PN:hypothetical protein Rv3737] [GN:Rv3737] [OR:Mycobacterium tuberculosis] [DB:genpept] [DE:Mycobacterium tuberculosis H37Rv complete genome; segment 155/162.] [NT:Rv3737, (MTV025.085), len: 529. Probable membrane] [LE:94796] [RE:96385] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_26359805_f1_11	3503	7275	168	55		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_26360663_c3_1530	3504	7276	1308	435	1039	5.9e-105

Description

pir: [LN:A70015] [AC:A70015] [PN:NADH dehydrogenase homolog yumB] [GN:yumB] [CL:NADH dehydrogenase] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1184289:g2635707] [LN:BSUB0017] [AC:Z99120:AL009126] [GN:yumB] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 17 of 21): from 3197001 to 3414420.] [NT:similar to NADH dehydrogenase] [LE:102091] [RE:103311] [DI:complement] >gp: [GI:e311467:g1934829] [LN:BSZ93939] [AC:Z93939] [PN:NADH dehydrogenase] [GN:yumB] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B. subtilis genomic DNA fragment from yumA to yulf.] [NT:putative; unknown] [LE:528] [RE:1748] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_26367175_c3_1476	3505	7277	123	40		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_26376077_c1_1113	3506	7278	192	63	101	1.5e-05

#### Description

pir: [LN:C70063] [AC:C70063] [PN:hypothetical protein ywmG] [GN:ywmG] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e276829:g1648859] [LN:BSATPC] [AC:Z81356] [PN:unknown] [GN:ywmH] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B. subtilis atpC gene.] [LE:10910] [RE:11098] [DI:direct] >gp: [GI:e1184573:g2636192] [LN:BSUB0019] [AC:Z99122:AL009126] [GN:ywmG] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091 to 3809700.] [LE:172069] [RE:172257] [DI:complement] >gp: [GI:e1184573:g2636192] [LN:BSUB0019] [AC:Z99122:AL009126] [GN:ywmG] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept] [DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091 to 3809700.] [LE:172069] [RE:172257] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_26464707_c3_1493	3507	7279	141	46	43	0.039

#### Description

pir: [LN:S58357] [AC:S66652:S58357] [PN:pepI protein] [GN:pepI] [OR:Staphylococcus epidermidis] [DB:pir2] >gp: [GI:g945016] [LN:SEPEPGNS] [AC:Z49865] [PN:PepI] [GN:pepI] [OR:Staphylococcus epidermidis] [DB:genpept-bct1] [DE:S. epidermidis pepA, pepB, pepC, pepI, pepP and pepT genes.] [LE:2028] [RE:2237] [DI:direct] >gp: [GI:g398082] [LN:STAPEPA] [AC:L23967] [PN:immunity protein] [GN:pepI] [OR:Staphylococcus epidermidis] [SR:Staphylococcus epidermidis DNA] [DB:genpept-bct1] [DE:Staphylococcus epidermidis lantibiotic (pepA) and immunity protein(pepI) gene, complete cds.] [LE:377] [RE:586] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_26578577_c1_1065	3508	7280	1791	596	2276	1.8e-238

#### Description

sp: [LN:UVRA\_BACSU] [AC:O34863] [GN:UVRA] [OR:BACILLUS SUBTILIS] [DE:EXCINUCLEASE ABC SUBUNIT A] [SP:O34863] [DB:swissprot] >pir: [LN:F69729] [AC:F69729] [PN:excinuclease ABC chain A:excision endonuclease ABC,, chain A:uvrA protein] [GN:uvrA] [CL:excinuclease ABC chain A:ATP-binding cassette homology] [OR:Bacillus subtilis] [EC:3.1.-.-] [DB:pir2] >gp: [GI:e1184422:g2636042] [LN:BSUB0019] [AC:Z99122:AL009126] [PN:excinuclease ABC (subunit A)] [GN:uvrA] [FN:excision of ultraviolet light-induced] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091 to 3809700.] [SP:O34863] [LE:12034] [RE:14907] [DI:complement] >gp: [GI:g2618842] [LN:AF017113] [AC:AF017113] [PN:excinuclease ABC subunit A] [GN:uvrA] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis 300-304 degree genomic sequence.] [LE:15386] [RE:18259] [DI:direct] >gp: [GI:e1184422:g2636042] [LN:BSUB0019] [AC:Z99122:AL009126] [PN:excinuclease ABC (subunit A)] [GN:uvrA] [FN:excision of ultraviolet light-induced] [OR:Bacillus subtilis] [DB:genpept] [DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091 to 3809700.] [SP:O34863] [LE:12034] [RE:14907] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_26594050_c3_1524	3509	7281	243	80	378	6.5e-35

Description

gp: [GI:d1013748:g1405337] [LN:D86240] [AC:D86240] [PN:D-alanyl carrier protein] [GN:dltC] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus (isolate:KAN96) DNA] [DB:genpept-bct1] [DE:Staphylococcus aureus gene for unkown function and dlt operon dltA, dltB, dltC and dltD genes, complete cds.] [NT:Sequence homologous to the dltC genes of] [LE:5303] [RE:5539] [DI:direct] >gp: [GI:g4530243] [LN:AF101234] [AC:AF101234] [PN:D-alanine carrier protein DltC] [GN:dltC] [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus dltABCD operon, complete sequence; andunkown gene.] [LE:4276] [RE:4512] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_26735877_c3_1508	3510	7282	402	133	446	4.1e-42

Description

pir: [LN:A70021] [AC:A70021] [PN:glycine cleavage system protein H homolog yusH] [GN:yusH] [CL:glycine cleavage system protein H: lipoyl/biotin-binding homology] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1184358:g2635776] [LN:BSUB0017] [AC:Z99120:AL009126] [GN:yusH] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.] [NT:similar to glycine cleavage system protein H] [LE:168182] [RE:168565] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_26753150_f1_147	3511	7283	336	111	295	4.1e-26

Description

sp: [LN:YKI4\_YEAST] [AC:P36078] [GN:YKL084W] [OR:SACCHAROMYCES CEREVISIAE] [SR:, BAKER'S YEAST] [DE:HYPOTHETICAL 13.6 KD PROTEIN IN MDH1-VMA5 INTERGENIC REGION] [SP:P36078] [DB:swissprot] >pir: [LN:S37909] [AC:S37909] [PN:hypothetical protein YKL084w] [OR:Saccharomyces cerevisiae] [DB:pir2] [MP:11L] >gp: [GI:g486123] [LN:SCYKL084W] [AC:Z28084:Y13137] [OR:Saccharomyces cerevisiae] [SR:baker's yeast] [DB:genpept-pln1] [DE:S.cerevisiae chromosome XI reading frame ORF YKL084w.] [NT:ORF YKL084w] [SP:P36078] [LE:382] [RE:732] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_26757807_f2_578	3512	7284	951	316	1619	2.0e-166

Description

gp: [GI:e255529:g1617430] [LN:SEABCTS] [AC:X99127] [PN:lipoprotein] [FN:iron repressible ABC transport system] [OR:Staphylococcus epidermidis] [DB:genpept-bct1] [DE:S.epidermidis gene encoding ABC transport system.] [LE:1621] [RE:2550] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_26834387_f1_234	3513	7285	711	236	115	1.2e-06

Description

gp: [GI:g3043880] [LN:LLU95841] [AC:U95841] [PN:transmembrane protein Tmp6] [OR:Lactococcus lactis] [DB:genpept-bct2] [DE:Lactococcus lactis transmembrane protein Tmp6 gene, partial cds.] [NT:identified as a fusion to a signal peptide-less] [LE:<1] [RE:354] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_26839462_c3_1474	3514	7286	1011	336	817	2.0e-81

Description

sp: [LN:YVCK\_BACSU] [AC:O06974] [GN:YVCK] [OR:BACILLUS SUBTILIS] [DE:HYPOTHETICAL 34.7 KD PROTEIN IN CRH-TRXB INTERGENIC REGION] [SP:O06974] [DB:swissprot]  
 >gp: [GI:e313027:g1945651] [LN:BSZ94043] [AC:Z94043] [PN:hypothetical protein] [GN:yvcK]  
 [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B. subtilis genomic DNA fragment (88 kb).]  
 [NT:similar to hypothetical SYCSLRA] [SP:O06974] [LE:10662] [RE:11615] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_2752262_c3_1426	3515	7287	1014	337	652	6.0e-64

Description

pir: [LN:G69669] [AC:G69669] [PN:choline ABC transporter (ATP-binding protein) opuBA] [GN:opuBA] [CL:glycine betaine/proline transport protein proV: ATP-binding cassette homology: CBS homology] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1186061:g2635886] [LN:BSUB0018] [AC:Z99121:AL009126] [PN:choline ABC transporter (ATP-binding protein)] [GN:opuBA] [FN:high affinity transport of choline] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.] [NT:alternate gene name: proV] [LE:61618] [RE:62763] [DI:complement] >gp: [GI:g2293447] [LN:AF008930] [AC:AF008930] [PN:ATPase] [GN:opuBA] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis choline transport system including ATPase(opuBA), transmembrane protein (opuBB), choline binding protein precursor (opuBC) and transmembrane protein (opuBD) genes, completecds; and unknown gene.] [NT:OpuBA; part of choline uptake system] [LE:881] [RE:2026] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_275268_c2_1225	3516	7288	1125	374	766	5.0e-76

Description

sp: [LN:HIS8\_BACSU] [AC:P17731:O32008] [GN:HISC:HISH] [OR:BACILLUS SUBTILIS] [EC:2.6.1.9] [DE:PHOSPHATE TRANSAMINASE)] [SP:P17731:O32008] [DB:swissprot]  
 >pir: [LN:A26532] [AC:A26532:G22794:H69640] [PN:histidinol-phosphate transaminase, / tyrosine and phenylalanine aminotransferase hisC:histidinol-phosphate aminotransferase] [GN:hisC:hish] [CL:probable histidinol-phosphate transaminase] [OR:Bacillus subtilis] [EC:2.6.1.9] [DB:pir2] [MP:205 (degrees)] >gp: [GI:g143814] [LN:BACVARGNS] [AC:M80245:M15409] [PN:HisH] [GN:hisH] [OR:Bacillus subtilis] [SR:Bacillus subtilis DNA] [DB:genpept-bct1] [DE:B. subtilis dbpA, mtr(A,B), gerC(1-3), ndk, cheR, aro(B,E,F,H), trp(A-F), hisH, and tyrA genes, complete cds.] [LE:14250] [RE:15332] [DI:direct] >gp: [GI:e1183707:g2634680] [LN:BSUB0012] [AC:Z99115:AL009126] [PN:tyrosine/phenylalanine aminotransferase] [GN:hisC] [FN:histidine biosynthesis] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:2.6.1.9:2.6.1.5] [DE:Bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.] [NT:alternate gene name: aroJ; histidinol-phosphate] [SP:P17731] [LE:174116] [RE:175198] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_2917200_f1_277	3517	7289	192	63		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_2926425_f2_465	3518	7290	960	319	456	3.5e-43

Description

sp: [LN:BMRU\_BACSU] [AC:P39074] [GN:BMRU] [OR:BACILLUS SUBTILIS] [DE:BMRU PROTEIN] [SP:P39074] [DB:swissprot] >pir: [LN:F69595] [AC:F69595] [PN:multidrug resistance protein cotranscribed with bmr bmrU] [GN:bmrU] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:g409286] [LN:BACBMRURBE] [AC:L25604] [GN:bmrU] [FN:unknown, but cotranscribed with bmr] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis bmrU, multidrug efflux transporter (bmr) and itsregulator (bmrR) genes, complete cds, and branched-chain 2-oxo aciddehydrogenase (bfmB) gene, 3' end.] [LE:227] [RE:1120] [DI:direct] >gp: [GI:d1013282:g1303947] [LN:BACJH642] [AC:D84432:D82370] [PN:BmrU] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:JH642(trpC2 PheA1)) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis DNA, 283 Kb region containing skin element.] [LE:225092] [RE:225985] [DI:complement] >gp: [GI:e1185668:g2634834] [LN:BSUB0013] [AC:Z99116:AL009126] [PN:multidrug resistance protein] [GN:bmrU] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.] [SP:P39074] [LE:97634] [RE:98527] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_2929517_c3_1399	3519	7291	126	41		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_29376503_f2_504	3520	7292	246	81		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_29378425_f3_790	3521	7293	132	43		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_29501510_c1_950	3522	7294	1125	374	432	1.2e-40

Description

sp: [LN:TAGB\_BACSU] [AC:P27621] [GN:TAGB] [OR:BACILLUS SUBTILIS] [DE:TEICHOIC ACID BIOSYNTHESIS PROTEIN B PRECURSOR] [SP:P27621] [DB:swissprot] >pir: [LN:C49757] [AC:C49757:C69720] [PN:polyglycerol phosphate techoic acid biosynthesis protein tagB] [GN:tagB] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:g143725] [LN:BACTAGABCD] [AC:M57497] [GN:tagB] [OR:Bacillus subtilis] [SR:B. subtilis (strain 168) DNA] [DB:genpept-bct1] [DE:B. subtilis tagA, tagB, tagC and tagD genes, complete cds.] [NT:putative] [LE:1603] [RE:2748] [DI:direct] >gp: [GI:e1184482:g2636102] [LN:BSUB0019] [AC:Z99122:AL009126] [GN:tagB] [FN:polyglycerol phosphate assembly and export] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.] [SP:P27621] [LE:84143] [RE:85288] [DI:direct] >gp: [GI:e1184482:g2636102] [LN:BSUB0019] [AC:Z99122:AL009126] [GN:tagB] [FN:polyglycerol phosphate assembly and export] [OR:Bacillus subtilis] [DB:genpept] [DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.] [SP:P27621] [LE:84143] [RE:85288] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_29570877_c3_1414	3523	7295	153	50		

Description

NO-HIT

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_3001313_c2_1262	3524	7296	681	226	154	3.6e-11

Description

pir: [LN:A65001] [AC:A65001] [PN:hypothetical protein b2291] [OR:Escherichia coli] [DB:pir2] >gp: [GI:g1788628] [LN:AE000318] [AC:AE000318:U00096] [PN:putative alpha helix protein] [GN:b2291] [FN:phenotype; Not classified] [OR:Escherichia coli] [DB:genpept-bct2] [DE:Escherichia coli K-12 MG1655 section 208 of 400 of the complete genome.] [NT:o199] [LE:4988] [RE:5587] [DI:direct]

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_30198587_f3_629	3525	7297	258	85	306	2.8e-27

Description

pir: [LN:C70024] [AC:C70024] [PN:NifU protein homolog homolog yutI] [GN:yutI] [CL:conserved hypothetical nifU-like protein HP1492] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1184301:g2635719] [LN:BSUB0017] [AC:Z99120:AL009126] [GN:yutI] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 17 of 21): from 3197001 to 3414420.] [NT:similar to NifU protein homolog] [LE:112444] [RE:112779] [DI:direct]

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_30265692_c3_1521	3526	7298	1050	349	1070	3.1e-108

Description

gp: [GI:g4530240] [LN:AF101234] [AC:AF101234] [PN:unknown] [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus dltABCD operon, complete sequence; and unknown gene.] [NT:Orf1; similar to hydroxyacid dehydrogenases] [LE:51] [RE:1010] [DI:direct]

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_30272661_f1_265	3527	7299	174	57		

Description

NO-HIT

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_30491275_c1_961	3528	7300	1104	367	391	2.7e-36

Description

pir: [LN:H69867] [AC:H69867] [PN:conserved hypothetical protein ykvI] [GN:ykvI] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1184961:g2633742] [LN:BSUB0008] [AC:Z99111:AL009126] [GN:ykvI] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 8 of 21): from 1394791 to 1603020.] [NT:similar to hypothetical proteins from B. subtilis] [LE:42768] [RE:43811] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_30601588_c3_1356	3529	7301	834	277	561	2.6e-54

Description

sp: [LN:TAGG\_BACSU] [AC:P42953] [GN:TAGG] [OR:BACILLUS SUBTILIS] [DE:TEICHOIC ACID TRANSLOCATION PERMEASE PROTEIN TAGG] [SP:P42953] [DB:swissprot] >pir: [LN:S69202] [AC:S69202:H69720] [PN:teichoic acid permease tagG:integral membrane protein tagG] [GN:tagG] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:g755152] [LN:BSU13832] [AC:U13832] [PN:highly hydrophobic integral membrane protein] [GN:tagG] [FN:teichoic acid translocation] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis 168 highly hydrophobic integral membrane protein(tagG) gene and ATP-binding protein (tagH) gene, complete cds.] [LE:287] [RE:1114] [DI:direct] >gp: [GI:e1184477:g2636097] [LN:BSUB0019] [AC:Z99122:AL009126] [PN:permease] [GN:tagG] [FN:teichoic acid translocation] [OR:Bacillus subtilis] [DB:genpept] [DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091 to 3809700.] [SP:P42953] [LE:77137] [RE:77964] [DI:complement] >gp: [GI:e1184477:g2636097] [LN:BSUB0019] [AC:Z99122:AL009126] [PN:permease] [GN:tagG] [FN:teichoic acid translocation] [OR:Bacillus subtilis] [DB:genpept] [DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091 to 3809700.] [SP:P42953] [LE:77137] [RE:77964] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_30661260_c1_1080	3530	7302	132	43		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_30745328_c1_1103	3531	7303	606	201	200	4.8e-16

Description

pir: [LN:S56619] [AC:S56619:B65255] [PN:gpmB protein:hypothetical protein o215b] [GN:gpmB] [CL:phosphoglycerate mutase homology] [OR:Escherichia coli] [DB:pir2] >gp: [GI:g537235] [LN:ECOUW93] [AC:U14003] [OR:Escherichia coli] [DB:genpept-bct1] [DE:Escherichia coli K-12 chromosomal region from 92.8 to 00.1 minutes.] [NT:Kenn Rudd identifies as gpmB] [LE:324630] [RE:325277] [DI:direct] >gp: [GI:g1790856] [LN:AE000509] [AC:AE000509:U00096] [PN:phosphoglyceromutase 2] [GN:gpmB] [FN:enzyme; Energy metabolism, carbon: Glycolysis] [OR:Escherichia coli] [DB:genpept-bct2] [DE:Escherichia coli K-12 MG1655 section 399 of 400 of the complete genome.] [LE:8985] [RE:9632] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_31257943_c2_1156	3532	7304	414	137	669	9.5e-66

Description

gp: [GI:g1913907] [LN:SAU91741] [AC:U91741] [PN:TagD] [GN:tagD] [FN:teichoic acid biosynthesis] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:Staphylococcus aureus teichoic acid biosynthesis TagB gene, partial cds and TagX and TagD genes, complete cds.] [NT:similar to Bacillus subtilis TagD] [LE:1534] [RE:1932] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_31267503_c2_1168	3533	7305	813	270	784	6.2e-78

Description

pir: [LN:A70001] [AC:A70001] [PN:ABC transporter (ATP-binding protein) homolog ytsC] [GN:ytsC] [CL:ATP-binding cassette homology] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1185911:g2635522] [LN:BSUB0016] [AC:Z99119:AL009126] [GN:ytsC] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 16 of 21): from 2997771 to 3213410.] [NT:similar to ABC transporter (ATP-binding protein)] [LE:112638] [RE:113399] [DI:complement] >gp: [GI:g2293177] [LN:AF008220] [AC:AF008220] [PN:transporter] [GN:ytsC] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis rrnB-dnaB genomic region.] [LE:67028] [RE:67789] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_31289687_c1_1051	3534	7306	681	226	132	5.1e-06

Description

gp: [GI:g4894306] [LN:AF065404] [AC:AF065404] [PN:pXO1-90] [OR:Bacillus anthracis] [DB:genpept-bct2] [DE:Bacillus anthracis virulence plasmid PXO1, complete sequence.] [LE:106772] [RE:108730] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_31428188_f2_401	3535	7307	222	73		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_31578_c2_1265	3536	7308	537	178	463	6.4e-44

Description

pir: [LN:H70044] [AC:H70044] [PN:O-acetyltransferase homolog yvoF] [GN:yvoF] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1186184:g2636009] [LN:BSUB0018] [AC:Z99121:AL009126] [GN:yvoF] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 18 of 21): from 3399551 to 3609060.] [NT:similar to O-acetyltransferase] [LE:190798] [RE:191316] [DI:complement] >gp: [GI:g2618861] [LN:AF017113] [AC:AF017113] [PN:putative acetyltransferase] [GN:yvoF] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis 300-304 degree genomic sequence.] [LE:36517] [RE:37035] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_31803377_f3_884	3537	7309	612	203		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_31876563_c1_1124	3538	7310	1239	412	1924	9.7e-199

Description

gp: [GI:d1013747:g1405336] [LN:D86240] [AC:D86240] [PN:hypothethcal membrane transporter] [GN:dltB] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus (isolate:KAN96) DNA] [DB:genpept-bct1] [DE:Staphylococcus aureus gene for unkown function and dlt operon dltA,dltB, dltC and dltD genes,complete cds,] [NT:Sequence homologous to the dltB genes of] [LE:4071] [RE:5285] [DI:direct] >gp: [GI:g4530242] [LN:AF101234] [AC:AF101234] [PN:putative membrane protein DltB] [GN:dltB] [FN:involved in D-alanine transfer into teichoic] [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus dltABCD operon, complete sequence; andunkown gene.] [LE:3044] [RE:4258] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_32062553_c1_943	3539	7311	468	155	354	2.3e-32

Description

pir: [LN:S61393] [AC:S61393] [PN:hypothetical protein 2] [OR:Bacillus sp.] [SR:strain C-125, , strain C-125] [SR:strain C-125, ] [DB:pir2] >gp: [GI:d1007182:g854656] [LN:BACAPS] [AC:D31823] [PN:ORF2] [OR:Bacillus sp.] [SR:Bacillus sp. (strain:C-125) DNA] [DB:genpept-bct1] [DE:Bacillus sp. Na+/H+ antiporter system responsible genes.] [NT:Na+/H+ antiporter system responsible gene] [LE:2669] [RE:3109] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_32070827_f3_789	3540	7312	168	55		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_32212902_c2_1135	3541	7313	1035	344	468	1.9e-44

Description

pir: [LN:F70046] [AC:F70046] [PN:iron permease homolog yvrB] [GN:yvrB] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1249808:g2832812] [LN:BS43KBDNA] [AC:AJ223978] [PN:putative hemin permease, YvrB] [GN:yvrB] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis 42.7kB DNA fragment from yvsA to yvqA.] [LE:24699] [RE:25760] [DI:direct] >gp: [GI:e1184396:g2635814] [LN:BSUB0017] [AC:Z99120:AL009126] [GN:yvrB] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.] [NT:similar to iron permease] [LE:204527] [RE:205588] [DI:complement] >gp: [GI:e1186005:g2635830] [LN:BSUB0018] [AC:Z99121:AL009126] [GN:yvrB] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.] [NT:similar to iron permease] [LE:1977] [RE:3038] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_32225012_f1_54	3542	7314	498	165	276	4.2e-24

Description

pir: [LN:F69870] [AC:F69870] [PN:general stress protein homolog ykzA] [GN:ykzA] [CL:hypothetical protein yk1A] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1181516:g2632036] [LN:BSAJ2571] [AC:AJ002571] [PN:YknA] [GN:yknA] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis 168 56 kb DNA fragment between xlyA and ykoR.] [NT:homologous to OsmC from Escherichia coli] [LE:34145] [RE:34555] [DI:direct] >gp: [GI:e1183336:g2633670] [LN:BSUB0007] [AC:Z99110:AL009126] [GN:ykzA] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.] [NT:alternate gene name: yzzE; similar to general] [LE:187094] [RE:187504] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_32475037_f3_651	3543	7315	123	40		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_32611068_c1_927	3544	7316	1674	557	1694	2.3e-174

Description

sp: [LN:SYR\_BACSU] [AC:P46906] [GN:ARGS] [OR:BACILLUS SUBTILIS] [EC:6.1.1.19] [DE:ARGINYL-TRNA SYNTHETASE, (ARGININE--TRNA LIGASE) (ARGRS)] [SP:P46906] [DB:swissprot] >pir: [LN:E69589] [AC:E69589:S60082] [PN:arginine--tRNA ligase, argS:arginyl-tRNA synthetase] [GN:argS] [CL:Bacillus arginine--tRNA ligase] [OR:Bacillus subtilis] [EC:6.1.1.19] [DB:pir2] >gp: [GI:e1186234:g2636270] [LN:BSUB0020] [AC:Z99123:AL009126] [PN:arginyl-tRNA synthetase] [GN:argS] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:6.1.1.19] [DE:Bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.] [SP:P46906] [LE:34303] [RE:35973] [DI:complement] >gp: [GI:e324388:g2224756] [LN:BSZ97024] [AC:Z97024] [PN:arginyl tRNA synthetase] [GN:argS] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis ywiA, swo, ywiB, argS and narK genes.] [SP:P46906] [LE:1680] [RE:3350] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_33210952_f2_370	3545	7317	234	77	93	0.0025

Description

gp: [GI:g3859891] [LN:AF072678] [AC:AF072678] [PN:alpha-actinin] [GN:AACTI] [OR:Trichomonas vaginalis] [DB:genpept-inv2] [DE:Trichomonas vaginalis alpha-actinin (AACTI) mRNA, complete cds.] [NT:actin binding protein] [LE:247] [RE:3042] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_33239001_f2_356	3546	7318	276	91		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_33304063_f1_151	3547	7319	159	52		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_33414143_c3_1395	3548	7320	1710	569	619	1.9e-60

Description

gp: [GI:g2773332] [LN:AF040718] [AC:AF040718] [PN:ABC transporter CydC] [GN:cydC] [OR:Shigella flexneri] [DB:genpept-bct2] [DE:Shigella flexneri ABC transporter CydC (cydC) gene, complete cds.] [NT:similar to E. coli CydC] [LE:1648] [RE:3369] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_33628441_f3_645	3549	7321	255	84		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_33645967_f1_18	3550	7322	282	93	73	0.019

Description

gp: [GI:g2444074] [LN:CPU88070] [AC:U88070] [GN:scc1] [FN:putative chaperone of type III secretory] [OR:Chlamydophila caviae] [DB:genpept-bct2] [DE:Chlamydophila caviae cds1, cds2, copN and scc1 genes, complete cds.] [NT:similar to SycE of Yersinia] [LE:4766] [RE:5206] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_34069680_c1_1125	3551	7323	213	70		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_34160625_c3_1368	3552	7324	438	145		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_34173262_c3_1497	3553	7325	141	46		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_34173385_c1_975	3554	7326	621	206	151	7.4e-11

Description

pir: [LN:E71040] [AC:E71040] [PN:hypothetical protein PH1613] [GN:PH1613] [OR:Pyrococcus horikoshii] [DB:pir2] >gp: [GI:d1031668:g3258042] [LN:AP000006] [AC:AP000006:AB005215:AB009510:AB009511:AB009512:AB009513:AB009514] [PN:166aa long hypothetical protein] [GN:PH1613] [OR:Pyrococcus horikoshii] [SR:Pyrococcus horikoshii (strain:OT3) DNA, clone:Pyrococcus horikoshi] [DB:genpept-bct1] [DE:Pyrococcus horikoshii OT3 genomic DNA, 1166001-1485000 nt. position(6/7).] [LE:263709] [RE:264209] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_34173750_c3_1485	3555	7327	480	159		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_34176550_f1_24	3556	7328	132	43		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_34189817_c1_945	3557	7329	2052	683	888	5.9e-89

Description

pir:[LN:E70040] [AC:E70040] [PN:conserved hypothetical protein yvgP] [GN:yvgP] [CL:hypothetical protein yvgP] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1186030:g2635855] [LN:BSUB0018] [AC:Z99121:AL009126] [GN:yvgP] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.] [NT:similar to hypothetical proteins] [LE:27843] [RE:29855] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_34242162_c3_1511	3558	7330	489	162	529	6.5e-51

Description

pir:[LN:E70019] [AC:E70019] [PN:NifU protein homolog homolog yurV] [GN:yurV] [CL:Yeast nitrogen fixation protein:nitrogen fixation protein homology] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1184346:g2635764] [LN:BSUB0017] [AC:Z99120:AL009126] [GN:yurV] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.] [NT:similar to NifU protein homolog] [LE:159070] [RE:159513] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_34251887_c2_1322	3559	7331	1266	421	1649	1.3e-169

Description

gp:[GI:g4530244] [LN:AF101234] [AC:AF101234] [PN:putative exoprotein DltD] [GN:dltD] [FN:involved in D-alanine transfer into teichoic] [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus dltABCD operon, complete sequence; and unknown gene.] [LE:4509] [RE:5684] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_34254581_c1_954	3560	7332	147	48		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_34261088_c3_1387	3561	7333	312	103	75	0.018

Description

gp:[GI:g488925] [LN:A13473] [AC:A13473] [PN:41kd antigen] [OR:Plasmodium falciparum] [SR:malaria parasite P. falciparum] [DB:genpept-pat] [DE:P.falciparum gene for 41kd antigen, clone 41-14.] [LE:<1] [RE:>532] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_34562762_c3_1336	3562	7334	750	249	230	3.2e-19

Description

pir: [LN:D71157] [AC:D71157] [PN:hypothetical protein PH0459] [GN:PH0459] [OR:Pyrococcus horikoshii] [DB:pir2] >gp: [GI:d1030488:g3256862] [LN:AP000002] [AC:AP000002:AB009475:AB009476:AB009477:AB009478:AB009479:AB009480] [PN:232aa long hypothetical protein] [GN:PH0459] [OR:Pyrococcus horikoshii] [SR:Pyrococcus horikoshii (strain:OT3) DNA] [DB:genpept-bct1] [DE:Pyrococcus horikoshii OT3 genomic DNA, 287001-544000 nt. position(2/7).] [LE:132975] [RE:133673] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_34571000_f1_163	3563	7335	537	178	393	1.7e-35

Description

sp: [LN:ADH2\_ENTHI] [AC:Q24803:Q27649] [GN:ADH2] [OR:ENTAMOEBA HISTOLYTICA] [EC:1.1.1.1:1.2.1.10] [DE:DEHYDROGENASE, (ACDH)] [SP:Q24803:Q27649] [DB:swissprot] >gp: [GI:g488430] [LN:EHU04863] [AC:U04863] [PN:alcohol dehydrogenase 2] [OR:Entamoeba histolytica] [DB:genpept-inv1] [DE:Entamoeba histolytica HM1:IMSS alcohol dehydrogenase 2 (EhADH2)mRNA, complete cds.] [NT:The derived amino acid sequence of EhADH2 is] [LE:3] [RE:2615] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_34589027_c2_1197	3564	7336	315	104	98	0.00023

Description

sp: [LN:Y420\_METJA] [AC:Q57863] [GN:MJ0420] [OR:METHANOCOCCUS JANNASCHII] [DE:HYPOTHETICAL PROTEIN MJ0420] [SP:Q57863] [DB:swissprot] >pir: [LN:D64352] [AC:D64352] [PN:hypothetical protein MJ0420] [OR:Methanococcus jannaschii] [DB:pir2] [MP:FOR378394-379536] >gp: [GI:g1591123] [LN:U67494] [AC:U67494:L77117] [PN:O-antigen polymerase isolog] [GN:MJ0420] [OR:Methanococcus jannaschii] [DB:genpept-bct2] [DE:Methanococcus jannaschii section 36 of 150 of the complete genome.] [NT:similar to GB:M60066 SP:P26479 PID:154343 percent] [LE:1855] [RE:2997] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_34612887_f2_512	3565	7337	465	154	260	2.1e-22

Description

pir: [LN:E69857] [AC:E69857] [PN:conserved hypothetical protein ykmA] [GN:ykmA] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1181515:g2632035] [LN:BSAJ2571] [AC:AJ002571] [PN:YkmA] [GN:ykmA] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis 168 56 kb DNA fragment between xlyA and ykoR.] [LE:33559] [RE:34002] [DI:complement] >gp: [GI:e1183335:g2633669] [LN:BSUB0007] [AC:Z99110:AL009126] [GN:ykmA] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.] [NT:similar to hypothetical proteins] [LE:186508] [RE:186951] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_34627136_f3_681	3566	7338	306	101	73	0.014

Description

pir: [LN:S36690] [AC:S36690] [PN:hypothetical protein] [OR:Autographa californica nuclear polyhedrosis virus:AcMNPV] [DB:pir2] >gp: [GI:g296321] [LN:ACNPVDNA] [AC:X71415] [GN:ORF 339] [OR:Autographa californica nucleopolyhedrovirus] [DB:genpept-vrl] [DE:Autographa californica nuclear polyhedrosis virus DNA.] [SP:Q06669] [LE:<1] [RE:339] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_34641875_c3_1406	3567	7339	939	312	704	1.9e-69

Description

pir:[LN:A69627] [AC:A69627] [PN:fructose 1-phosphate kinase fruB] [GN:fruB] [CL:6-phosphofructokinase 2] [OR:Bacillus subtilis] [DB:pir2]  
>gp:[GI:e1185029:g2633810] [LN:BSUB0008] [AC:Z99111:AL009126] [PN:fructose-1-phosphate kinase] [GN:fruB] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:2.7.1.56] [DE:Bacillus subtilis complete genome (section 8 of 21): from 1394791 to 1603020.] [LE:112945] [RE:113856] [DI:direct] >gp:[GI:g3282124] [LN:AF012285] [AC:AF012285:AF012284:U51911] [PN:fructose-1-phosphate kinase] [GN:fruB] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis mobA-nprE gene region.] [NT:similar to L. lactis tagatose-6-phosphate kinase,] [LE:13433] [RE:14344] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503001001_34642567_c1_1089	3568	7340	2406	801	2175	1.0e-228
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Description

pir:[LN:G70027] [AC:G70027] [PN:conserved hypothetical protein yvaJ] [GN:yvaJ] [CL:virulence-associated protein vacB homolog] [OR:Bacillus subtilis] [DB:pir2]  
>gp:[GI:e1186049:g2635874] [LN:BSUB0018] [AC:Z99121:AL009126] [GN:yvaJ] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 18 of 21): from 3399551 to 3609060.] [NT:similar to hypothetical proteins] [LE:51375] [RE:53714] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503001001_34645311_f3_867	3569	7341	525	174	186	1.4e-14
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Description

gp:[GI:g4981094] [LN:AE001732] [AC:AE001732:AE000512] [PN:conserved hypothetical protein] [GN:TM0577] [OR:Thermotoga maritima] [DB:genpept-bct2] [DE:Thermotoga maritima section 44 of 136 of the complete genome.] [NT:similar to SP:P46854 PID:606376 GB:U00096] [LE:9820] [RE:10359] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503001001_3518_f2_375	3570	7342	159	52		
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503001001_35422880_c2_1228	3571	7343	129	42		
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_35444127_f2_443	3572	7344	663	220	514	2.5e-49

Description

sp: [LN:YVYE\_BACSU] [AC:P32437:P96500] [GN:YVYE:YVHK] [OR:BACILLUS SUBTILIS] [DE:HYPOTHETICAL 24.8 KD PROTEIN IN DEGS-TAGO INTERGENIC REGION] [SP:P32437:P96500] [DB:swissprot] >pir: [LN:A70049] [AC:A70049:A30191] [PN:conserved hypothetical protein yvyE] [GN:yvyE] [CL:hypothetical protein HI0722] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1184457:g2636077] [LN:BSUB0019] [AC:Z99122:AL009126] [GN:yvyE] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.] [NT:alternate gene name: yvhK; similar to hypothetical] [SP:P32437] [LE:48723] [RE:49376] [DI:direct] >gp: [GI:g1762328] [LN:BSU56901] [AC:U56901] [PN:Ycr59c/YigZ homolog] [GN:yvhK] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis putative transcriptional regulator (yvhJ), Ycr59c/YigZ homolog (yvhK), histidine kinase (degS), transcriptional regulator of degradation enzyme (degU), (degV), (comFA), (comFB), (comFC), flagellar protein (yviB), negative regulator of flagellin(flgM), flagellar protein (yviC), flagellar-hook associated protein1 (flgK), flagellar-hook associated protein 3 (flgL), (yviE), transmembrane protein (yviF), (csrA), flagellin (hag), flagellarprotein (yviH), flagellar hook-associated protein 2 (fliD), flagellar protein (fliS), flagellar protein (fliT), sigma-54modulator homolog (yviI), and (secA) genes, complete cds.] [LE:1217] [RE:1870] [DI:complement] >gp: [GI:e1184457:g2636077] [LN:BSUB0019] [AC:Z99122:AL009126] [GN:yvyE] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept] [DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.] [NT:alternate gene name: yvhK; similar to hypothetical] [SP:P32437] [LE:48723] [RE:49376] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_35945277_c3_1463	3573	7345	1065	354	1275	5.8e-130

Description

sp: [LN:RF2\_BACSU] [AC:P28367:O34444] [GN:PRFB] [OR:BACILLUS SUBTILIS] [DE:PEPTIDE CHAIN RELEASE FACTOR 2 (RF-2)] [SP:P28367:O34444] [DB:swissprot] >pir: [LN:JN0146] [AC:H69681:JN0146] [PN:translation releasing factor RF-2:peptide chain release factor 2:prfB] [GN:prfB] [CL:translation releasing factor] [OR:Bacillus subtilis] [DB:pir1] >gp: [GI:e1184435:g2636055] [LN:BSUB0019] [AC:Z99122:AL009126] [PN:peptide chain release factor 2] [GN:prfB] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.] [SP:P28367] [LE:29109:30139] [RE:30137:30210] [DI:complementJoin] >gp: [GI:g2331287] [LN:AF013188] [AC:AF013188] [PN:release factor 2] [GN:prfB] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis release factor 2 (prfB) gene, complete cds.] [NT:orf3; naturally occurring frame-shift] [LE:75:148] [RE:146:1176] [DI:directJoin] >gp: [GI:g2618874] [LN:AF017113] [AC:AF017113] [PN:putative peptide chain release factor RF-2] [GN:prfB] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis 300-304 degree genomic sequence.] [LE:83:156] [RE:154:1184] [DI:directJoin] >gp: [GI:e1184435:g2636055] [LN:BSUB0019] [AC:Z99122:AL009126] [PN:peptide chain release factor 2] [GN:prfB] [OR:Bacillus subtilis] [DB:genpept] [DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.] [SP:P28367] [LE:29109:30139] [RE:30137:30210] [DI:complementJoin]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_35988961_f2_376	3574	7346	129	42		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_36131311_c3_1455	3575	7347	696	231	194	2.1e-15

Description

gp: [GI:g451867] [LN:BACFLGMK] [AC:L14437] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain W168) (library: lambda gtWES library] [DB:genpept-bct1] [DE:Bacillus subtilis (clones pDM116 and pDM113) flagellin synthesisregulatory protein (flgM) and flagellar hook-filament junctionprotein (flgK) genes and orf139, orf160, orfX, complete cds's.] [NT:in Z18629, ORFX is called comForf3; ORFX; putative] [LE:<1] [RE:754] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_36133385_c3_1377	3576	7348	681	226	203	2.3e-16

Description

pir: [LN:G69798] [AC:G69798] [PN:hypothetical protein yetJ] [GN:yetJ] [CL:hypothetical protein yetJ] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1182699:g2633033] [LN:BSUB0004] [AC:Z99107:AL009126] [GN:yetJ] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 4 of 21): from 600701 to 813890.] [LE:186800] [RE:187444] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_36229676_c1_936	3577	7349	795	264	238	4.5e-20

Description

gp: [GI:g3172115] [LN:ACCPAOP] [AC:L05770:U04359:M33798:U20284:U11554:L13114:L03407] [PN:beta-keto adipate enol-lactone hydrolase] [GN:pcaD] [OR:Acinetobacter sp. ADP1] [DB:genpept-bct2] [EC:3.1.1.24] [DE:Acinetobacter sp. ADP1 pca-qui-pob supraoperonic cluster, complete sequence.] [NT:ELH] [LE:6843] [RE:7643] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_36230252_c1_1000	3578	7350	777	258	480	1.0e-45

Description

pir: [LN:B69627] [AC:B69627] [PN:transcription repressor of fructose operon fruR] [GN:fruR] [CL:regulatory protein gutR] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1185028:g2633809] [LN:BSUB0008] [AC:Z99111:AL009126] [PN:transcriptional regulator (DeoR family)] [GN:fruR] [FN:negative regulation of the fructose operon] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 8 of 21): from 1394791 to 1603020.] [LE:112193] [RE:112948] [DI:direct] >gp: [GI:g3282123] [LN:AF012285] [AC:AF012285:AF012284:U51911] [PN:FruR] [GN:fruR] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis mobA-nprE gene region.] [NT:similar to L. lactis lactose PTS system repressor,] [LE:12681] [RE:13436] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_36367302_c3_1330	3579	7351	564	187	122	2.7e-06

Description

sp: [LN:Y359\_METJA] [AC:Q57805] [GN:MJ0359] [OR:METHANOCOCCUS JANNASCHII] [DE:HYPOTHETICAL PROTEIN MJ0359] [SP:Q57805] [DB:swissprot] >pir: [LN:G64344] [AC:G64344] [PN:hypothetical protein MJ0359] [OR:Methanococcus jannaschii] [DB:pir2] [MP:REV327449-326805] >gp: [GI:g1591068] [LN:U67489] [AC:U67489:L77117] [PN:M. jannaschii predicted coding region MJ0359] [GN:MJ0359] [OR:Methanococcus jannaschii] [DB:genpept-bct2] [DE:Methanococcus jannaschii section 31 of 150 of the complete genome.] [NT:hypothetical protein; identified by GeneMark;] [LE:2497] [RE:3141] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_36563_c2_1302	3580	7352	1074	357	908	4.5e-91

Description

pir:[LN:D70020] [AC:D70020] [PN:ABC transporter (ATP-binding protein) homolog yusC] [GN:yusC] [CL:ATP-binding cassette homology] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1184353:g2635771] [LN:BSUB0017] [AC:Z99120:AL009126] [GN:yusC] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 17 of 21): from 3197001 to 3414420.] [NT:similar to ABC transporter (ATP-binding protein)] [LE:165325] [RE:166350] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_36601562_c3_1403	3581	7353	1182	393	1669	1.0e-171

Description

sp:[LN:NORA\_STAAU] [AC:P21191] [GN:NORA] [OR:STAPHYLOCOCCUS AUREUS] [DE:QUINOLONE RESISTANCE NORA PROTEIN] [SP:P21191] [DB:swissprot] >pir:[LN:A37838] [AC:A37838] [PN:norA protein] [OR:Staphylococcus aureus] [DB:pir2] >gp:[GI:d1014850:g216975] [LN:STANORA] [AC:D90119] [PN:ORF for norA] [GN:norA] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus (strain TK2566) genomic DNA] [DB:genpept-bct1] [DE:S. aureus norA gene.] [LE:478] [RE:1644] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_37927_f1_282	3582	7354	123	40		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_391527_f3_880	3583	7355	930	309	700	4.9e-69

Description

sp:[LN:TAGH\_BACSU] [AC:P42954] [GN:TAGH] [OR:BACILLUS SUBTILIS] [DE:TEICHOIC ACID TRANSLOCATION ATP-BINDING PROTEIN TAGH] [SP:P42954] [DB:swissprot] >pir:[LN:S69203] [AC:S69203:A69721] [PN:teichoic acid translocation ATP-binding protein tagH] [GN:tagH] [CL:ATP-binding cassette homology] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:g755153] [LN:BSU13832] [AC:U13832] [PN:ATP-binding protein] [GN:tagH] [FN:teichoic acid translocation] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis 168 highly hydrophobic integral membrane protein(tagG) gene and ATP-binding protein (tagH) gene, complete cds.] [LE:1134] [RE:2717] [DI:direct] >gp:[GI:e1184476:g2636096] [LN:BSUB0019] [AC:Z99122:AL009126] [PN:ATP-binding protein] [GN:tagH] [FN:teichoic acid translocation] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091 to 3809700.] [SP:P42954] [LE:75534] [RE:77117] [DI:complement] >gp:[GI:e1184476:g2636096] [LN:BSUB0019] [AC:Z99122:AL009126] [PN:ATP-binding protein] [GN:tagH] [FN:teichoic acid translocation] [OR:Bacillus subtilis] [DB:genpept] [DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091 to 3809700.] [SP:P42954] [LE:75534] [RE:77117] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_3922550_f1_67	3584	7356	138	45		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_3928762_f2_369	3585	7357	1368	455	839	9.2e-84

Description

pir:[LN:B70007] [AC:B70007] [PN:Na+-transporting ATP synthase homolog yubG] [GN:yubG] [CL:Na+-ATP synthase chain J] [OR:Bacillus subtilis] [DB:pir2]  
 >gp:[GI:e1185983:g2635594] [LN:BSUB0016] [AC:Z99119:AL009126] [GN:yubG] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 16 of 21): from 2997771 to 3213410.] [NT:similar to Na+-transporting ATP synthase] [LE:190389] [RE:191726] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_3939218_c1_922	3586	7358	135	44		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_3942263_c3_1381	3587	7359	726	241	913	1.3e-91

Description

pir:[LN:C69793] [AC:C69793] [PN:conserved hypothetical protein yeeI] [GN:yeeI] [CL:hypothetical protein MG332] [OR:Bacillus subtilis] [DB:pir2]  
 >gp:[GI:e1182664:g2632998] [LN:BSUB0004] [AC:Z99107:AL009126] [GN:yeeI] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 4 of 21): from 600701 to 813890.] [NT:similar to hypothetical proteins] [LE:151216] [RE:151938] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_3944001_c1_1130	3588	7360	1524	507	684	2.4e-67

Description

pir:[LN:F70012] [AC:F70012] [PN:leucyl aminopeptidase homolog yuiE] [GN:yuiE] [CL:cytosol aminopeptidase] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1184284:g2635702] [LN:BSUB0017] [AC:Z99120:AL009126] [GN:yuiE] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 17 of 21): from 3197001 to 3414420.] [NT:similar to leucyl aminopeptidase] [LE:98474] [RE:99976] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_3948587_f2_340	3589	7361	873	290	378	6.5e-35

Description

gp:[GI:g4980658] [LN:AE001701] [AC:AE001701:AE000512] [PN:conserved hypothetical protein] [GN:TM0164] [OR:Thermotoga maritima] [DB:genpept-bct2] [DE:Thermotoga maritima section 13 of 136 of the complete genome.] [NT:similar to GB:AE000666 percent identity: 61.11;] [LE:9393] [RE:10187] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_3953452_c2_1201	3590	7362	507	168	328	1.3e-29

Description

pir:[LN:D69849] [AC:D69849] [PN:transcription regulation homolog yjdI] [GN:yjdI] [CL:conserved hypothetical protein HI434] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1183226:g2633560] [LN:BSUB0007] [AC:Z99110:AL009126] [GN:yjdI] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 7 of 21): from 1194391 to 1411140.] [NT:similar to transcription regulation] [LE:82766] [RE:83245] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_3955067_c2_1278	3591	7363	126	41		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_3959377_f3_886	3592	7364	126	41	149	1.7e-10

Description

gp: [GI:e255528:g1617429] [LN:SEABCTS] [AC:X99127] [PN:membrane protein] [FN:iron repressible ABC transport system] [OR:Staphylococcus epidermidis] [DB:genpept-bct1] [DE:S.epidermidis gene encoding ABC transport system.] [LE:878] [RE:1624] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_3962915_f2_507	3593	7365	627	208	139	1.1e-08

Description

pir: [LN:C71375] [AC:C71375] [PN:conserved hypothetical integral membrane protein TP0033] [GN:TP0033] [OR:Treponema pallidum subsp. pallidum] [SR:, syphilis spirochete] [DB:pir2] >gp: [GI:g3322288] [LN:AE001188] [AC:AE001188:AE000520] [PN:conserved hypothetical integral membrane] [GN:TP0033] [OR:Treponema pallidum] [DB:genpept-bct2] [DE:Treponema pallidum section 4 of 87 of the complete genome.] [NT:similar to PID:1001613 PID:1001643 percent] [LE:7016] [RE:7627] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_39818_f2_530	3594	7366	240	79	234	1.2e-19

Description

gp: [GI:g1575061] [LN:SAU57060] [AC:U57060] [PN:ScdA] [GN:scdA] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:Staphylococcus aureus scdA gene, complete cds.] [NT:s. aureus cells containing a scdA disruption have] [LE:361] [RE:1035] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_3994027_f1_193	3595	7367	141	46		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_4023518_f2_400	3596	7368	909	302	579	3.3e-56

Description

pir: [LN:G69800] [AC:G69800] [PN:cell-division inhibitor homolog yfhF] [GN:yfhF] [CL:cell division inhibitor yfhF] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1182841:g2633175] [LN:BSUB0005] [AC:Z99108:AL009126] [GN:yfhF] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 5 of 21): from 802821 to 1011250.] [NT:similar to cell-division inhibitor] [LE:121320] [RE:122231] [DI:complement] >gp: [GI:d1025388:g2804536] [LN:D85082] [AC:D85082] [PN:YfhF] [OR:Bacillus subtilis] [SR:Bacillus subtilis DNA] [DB:genpept-bct1] [DE:Bacillus subtilis DNA, genome sequence, 79 to 81 degree region.] [LE:14211] [RE:15122] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_4036093_c3_1384	3597	7369	864	287	461	1.0e-43

Description

pir: [LN:B69866] [AC:B69866] [PN:transcription regulator LysR family homolog ykuM] [GN:ykuM] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1181918:g2632234] [LN:BS16829KB] [AC:AJ222587] [PN:YkuM protein] [GN:ykuM] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis 29kB DNA fragment from ykwC gene to cse15 gene.] [NT:homologous to LysR type transcriptional regulators] [LE:20403] [RE:21284] [DI:direct] >gp: [GI:e1185004:g2633785] [LN:BSUB0008] [AC:Z99111:AL009126] [GN:ykuM] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 8 of 21): from 1394791 to 1603020.] [NT:similar to transcriptional regulator (LysR family)] [LE:90659] [RE:91540] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_4072006_f3_845	3598	7370	201	66		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_4095055_f2_463	3599	7371	894	297	512	4.1e-49

Description

pir: [LN:B71256] [AC:B71256] [PN:conserved hypothetical integral membrane protein TP0986] [GN:TP0986] [OR:Treponema pallidum subsp. pallidum] [SR:, syphilis spirochete] [DB:pir2] >gp: [GI:g3323311] [LN:AE001266] [AC:AE001266:AE000520] [PN:conserved hypothetical integral membrane] [GN:TP0986] [OR:Treponema pallidum] [DB:genpept-bct2] [DE:Treponema pallidum section 82 of 87 of the complete genome.] [NT:similar to GB:AE000511 PID:2314395 percent] [LE:1967] [RE:2851] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_4096093_c3_1496	3600	7372	354	117	155	2.8e-11

Description

pir: [LN:B42573] [AC:B42573] [PN:urf120] [OR:Paracoccus denitrificans] [DB:pir2]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_4100093_c3_1419	3601	7373	1161	386	489	1.1e-46

Description

pir: [LN:E64556] [AC:E64556] [PN:para-aminobenzoate synthetase] [OR:Helicobacter pylori] [DB:pir2] >gp: [GI:g2313385] [LN:AE000547] [AC:AE000547:AE000511] [PN:para-aminobenzoate synthetase (pabB)] [GN:HP0293] [OR:Helicobacter pylori 26695] [DB:genpept-bct2] [DE:Helicobacter pylori 26695 section 25 of 134 of the complete genome.] [NT:similar to GB:K02673 SP:P05041 GB:U07748 GB:U07749] [LE:20379] [RE:22058] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_4101643_c2_1314	3602	7374	399	132	304	4.5e-27

Description

pir: [LN:F70023] [AC:F70023] [PN:hypothetical protein yutD] [GN:yutD] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1184310:g2635728] [LN:BSUB0017] [AC:Z99120:AL009126] [GN:yutD] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 17 of 21): from 3197001 to 3414420.] [LE:121344] [RE:121652] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_4103393_c2_1215	3603	7375	597	198	436	4.7e-41

Description

sp: [LN:PABA\_SALTY] [AC:P06193] [GN:PABA] [OR:Salmonella typhimurium] [EC:4.1.3.-] [DE:(EC 4.1.3.-) (ADC SYNTHASE)] [SP:P06193] [DB:swissprot] >pir:[LN:S09636] [AC:S09636] [PN:pabA protein] [GN:pabA] [CL:glutamine amidotransferase:trpG homology] [OR:Salmonella typhimurium] [DB:pir2] >gp:[GI:g47816] [LN:STPABA] [AC:X02603] [OR:Salmonella typhimurium] [DB:genpept-bct1] [DE:Salmonella typhimurium pabA gene for para-aminobenzoate synthase glutamine amidotransferase.] [NT:pabA gene product (aa 1-187)] [SP:P06193] [LE:1] [RE:564] [DI:direct] >gp:[GI:g154228] [LN:STYPABAA] [AC:M32355] [OR:Salmonella typhimurium] [SR:S.typhimurium DNA, clone pSZD3] [DB:genpept-bct1] [DE:S.typhimurium glutamine amidotransferase subunit of para-aminobenzoate synthase (pabA) and pot. cell division protein infic) genes, complete cds.] [NT:glutamine amidotransferase] [LE:970] [RE:1533] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_4110888_c3_1380	3604	7376	405	134	93	0.00010

Description

gp:[GI:g3283053] [LN:AF054173] [AC:AF054173] [PN:staphylococcal accessory regulator A homolog] [GN:sarA] [OR:Staphylococcus epidermidis] [DB:genpept-bct2] [DE:Staphylococcus epidermidis staphylococcal accessory regulator Ahomolog (sarA) gene, complete cds.] [LE:887] [RE:1261] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_4111691_c1_1018	3605	7377	744	247	351	1.5e-31

Description

sp: [LN:YCSJ\_BACSU] [AC:P42967] [GN:YCSJ] [OR:BACILLUS SUBTILIS] [DE:HYPOTHETICAL 63.8 KD PROTEIN IN SIPU-PBPC INTERGENIC REGION] [SP:P42967] [DB:swissprot] >pir:[LN:G69765] [AC:G69765:I39898] [PN:allophanate hydrolase homolog ycsJ:probable urea amidolyase] [GN:ycsJ] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:d1007939:g790943] [LN:BAC39R] [AC:D38161] [PN:urea amidolyase] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:168TrpC2) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis genome around 39 degrees region encoding 17 ORFs, complete cds.] [LE:10358] [RE:12094] [DI:direct] >gp:[GI:e1182375:g2632709] [LN:BSUB0003] [AC:Z99106:AL009126] [GN:ycsJ] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 3 of 21): from 402751 to 611850.] [NT:similar to allophanate hydrolase] [SP:P42967] [LE:56667] [RE:58403] [DI:direct] >gp:[GI:d1009674:g1805477] [LN:D50453] [AC:D50453] [PN:homologues to hypothetical protein HI1731 of H.] [GN:ycsJ] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:168 trpC2) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis DNA for 25-36 degree region containing theamyE-srfA region, complete cds.] [LE:139065] [RE:140801] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_4195817_c1_955	3606	7378	1743	580	2597	4.7e-270

Description

gp:[GI:e264711:g1262136] [LN:SAPBP4GEN] [AC:X91786] [PN:ATP-binding cassette transporter A] [GN:abcA] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:S.aureus abcA, pbp4, and tagD genes.] [LE:311] [RE:2038] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503001001_42167_c1_959	3607	7379	834	277	1083	1.3e-109
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Description

gp: [GI:g4928292] [LN:AF132117] [AC:AF132117] [PN:FhuA] [GN:fhuA] [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus ferrichrome uptake operon, complete sequence and unknown genes.] [NT:ATP binding protein.] [LE:2780] [RE:3514] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503001001_422162_f3_795	3608	7380	456	151	439	2.2e-41
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Description

pir: [LN:B69868] [AC:B69868] [PN:6-pyruvoyl tetrahydrobiopterin synthase homolog ykvK] [GN:ykvK] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1184963:g2633744] [LN:BSUB0008] [AC:Z99111:AL009126] [GN:ykvK] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 8 of 21): from 1394791 to 1603020.] [NT:similar to 6-pyruvoyl tetrahydrobiopterin synthase] [LE:44776] [RE:45225] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503001001_422800_f3_903	3609	7381	447	148	627	2.7e-61
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Description

gp: [GI:g3283053] [LN:AF054173] [AC:AF054173] [PN:staphylococcal accessory regulator A homolog] [GN:sarA] [OR:Staphylococcus epidermidis] [DB:genpept-bct2] [DE:Staphylococcus epidermidis staphylococcal accessory regulator A homolog (sarA) gene, complete cds.] [LE:887] [RE:1261] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503001001_425927_f1_232	3610	7382	144	47		
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503001001_429675_f2_558	3611	7383	216	71		
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503001001_4330390_c3_1517	3612	7384	876	291	787	3.0e-78
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Description

pir: [LN:A70016] [AC:A70016] [PN:hypothetical protein yunF] [GN:yunF] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1184318:g2635736] [LN:BSUB0017] [AC:Z99120:AL009126] [GN:yunF] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 17 of 21): from 3197001 to 3414420.] [LE:127975] [RE:128829] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503001001_4351465_c2_1159	3613	7385	129	42		
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_4461693_f2_596	3614	7386	240	79		

Description

NO-HIT

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_4487588_f3_797	3615	7387	609	202	81	0.00094

Description

pir:[LN:B69478] [AC:B69478] [PN:NADH dehydrogenase (ubiquinone),, 43.2 kDa subunit homolog] [OR:Archaeoglobus fulgidus] [EC:1.6.5.3] [DB:pir2] >gp:[GI:g2648717] [LN:AE000976] [AC:AE000976:AE000782] [PN:F420H2:quinone oxidoreductase, 43.2 kDa subunit,] [GN:AF1827] [OR:Archaeoglobus fulgidus] [DB:genpept-bct2] [DE:Archaeoglobus fulgidus section 131 of 172 of the complete genome.] [NT:similar to PID:882405 SP:P50973 percent identity:] [LE:4241] [RE:5455] [DI:direct]

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_4501250_c1_1097	3616	7388	1080	359	871	3.7e-87

Description

gp:[GI:d1020364:g1944409] [LN:D87026] [AC:D87026:D28136] [PN:membrane protein] [OR:Bacillus stearothermophilus] [SR:Bacillus stearothermophilus (strain:TRBE14) DNA] [DB:genpept-bct1] [DE:Bacillus stearothermophilus glycogen operon genes, complete cds.] [NT:The ORF is similar to the Alkaligenes eutrophus] [LE:144] [RE:1097] [DI:complement]

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_4511550_c2_1247	3617	7389	1278	425	318	1.5e-28

Description

sp:[LN:YHAD\_ECOLI] [AC:P23524] [GN:YHAD] [OR:ESCHERICHIA COLI] [DE:HYPOTHETICAL 39.1 KD PROTEIN IN RNPB-SOHA INTERGENIC REGION (ORF 3)] [SP:P23524] [DB:swissprot]

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_4535652_f1_255	3618	7390	225	74		

Description

NO-HIT

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_4539143_c1_1066	3619	7391	942	313	970	1.2e-97

Description

sp:[LN:HPRK\_BACSU] [AC:O34483] [GN:PTSK] [OR:BACILLUS SUBTILIS] [EC:2.7.1.-] [DE:HPR(SER) KINASE,] [SP:O34483] [DB:swissprot]

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_4578956_f1_101	3620	7392	297	98	79	0.021

Description

gp:[GI:e1350598:g3881046] [LN:CEY51A2D] [AC:AL021497] [GN:Y51A2D.12] [OR:Caenorhabditis elegans] [DB:genpept-inv1] [DE:Caenorhabditis elegans cosmid Y51A2D, complete sequence.] [LE:83074:83534:84872] [RE:83208:83768:84978] [DI:complementJoin]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_4687843_c2_1324	3621	7393	330	109	242	1.7e-20

Description

pir: [LN:C70026] [AC:C70026] [PN:hypothetical protein yuzD] [GN:yuzD] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1184300:g2635718] [LN:BSUB0017] [AC:Z99120:AL009126] [GN:yuzD] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 17 of 21): from 3197001 to 3414420.] [LE:112018] [RE:112344] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_4689077_c2_1271	3622	7394	333	110	466	3.1e-44

Description

sp: [LN:CLPP\_BACSU] [AC:P80244:O08433] [GN:CLPP] [OR:BACILLUS SUBTILIS] [EC:3.4.21.92] [DE:(ENDOPEPTIDASE CLP) (CASEINOLYTIC PROTEASE) (PROTEASE TI)] [SP:P80244:O08433] [DB:swissprot] >pir: [LN:B69601] [AC:B69601:A47683] [PN:ATP-dependent clp proteinase, chain P:stress protein G7] [GN:clpP] [CL:ATP-dependent Clp proteinase chain P] [OR:Bacillus subtilis] [EC:3.4.21.-] [DB:pir2] >gp: [GI:e1186142:g2635967] [LN:BSUB0018] [AC:Z99121:AL009126] [PN:ATP-dependent Clp protease proteolytic subunit] [GN:clpP] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:3.4.21.92] [DE:Bacillus subtilis complete genome (section 18 of 21): from 3399551 to 3609060.] [NT:alternate gene name: yvdN] [SP:P80244] [LE:145744] [RE:146337] [DI:direct] >gp: [GI:e313044:g1945673] [LN:BSZ94043] [AC:Z94043] [PN:hypothetical protein] [GN:yvdN] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B. subtilis genomic DNA fragment (88 kb).] [NT:similar to CLPP\_ECOLI ATP-dependent clp protease] [SP:P80244] [LE:35334] [RE:35927] [DI:complement] >gp: [GI:g2668494] [LN:BSU59754] [AC:U59754] [PN:ClpP] [GN:clpP] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis Clp protease proteolytic component (clpP) gene, complete cds.] [NT:proteolytic component of Clp protease] [LE:140] [RE:733] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_4689130_f2_614	3623	7395	306	101	81	0.029

Description

pir: [LN:A58932] [AC:A58932] [PN:cytochrome C-type biogenesis protein CCMF] [GN:yejR:ccmF] [OR:mitochondrion Cyanidioschyzon merolae] [DB:pir2] >gp: [GI:d1037513:g4115789] [LN:D89861] [AC:D89861] [PN:cytochrome C-type biogenesis protein CCMF] [GN:yejR or ccmF] [OR:Mitochondrion Cyanidioschyzon merolae] [SR:Cyanidioschyzon merolae (strain:10D) mitochondrial DNA] [DB:genpept-pln1] [DE:Cyanidioschyzon merolae mitochondrial DNA, complete sequence.] [LE:16296] [RE:18158] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_4695293_c3_1487	3624	7396	171	56		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_4703180_c1_1041	3625	7397	453	150	541	3.5e-52

Description

gp: [GI:e1393149:g4490608] [LN:SAU133495] [AC:AJ133495] [PN:NRD1] [GN:nrd1] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:Staphylococcus aureus ribonucleotide reductase operon.] [LE:138] [RE:536] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_4709575_c2_1309	3626	7398	354	117		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_4726462_f2_572	3627	7399	168	55		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_4726527_f3_774	3628	7400	528	175	749	3.2e-74

Description

pir:[LN:D69868] [AC:D69868] [PN:conserved hypothetical protein ykvM] [GN:ykvM] [CL:hypothetical protein ykvM] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1184965:g2633746] [LN:BSUB0008] [AC:Z99111:AL009126] [GN:ykvM] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 8 of 21): from 1394791 to 1603020.] [NT:similar to hypothetical proteins] [LE:45967] [RE:46464] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_4773392_f2_359	3629	7401	288	95		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_4775287_c3_1420	3630	7402	1008	335	238	1.3e-34

Description

sp:[LN:YBGK\_ECOLI] [AC:P75745] [GN:YBGK] [OR:ESCHERICHIA COLI] [DE:HYPOTHETICAL 34.4 KD PROTEIN IN PHRB-NEI INTERGENIC REGION] [SP:P75745] [DB:swissprot] >pir:[LN:G64806] [AC:G64806] [PN:ybgK protein] [GN:ybgK] [CL:hypothetical protein HI1730] [OR:Escherichia coli] [DB:pir2] >gp:[GI:d1036362:g4062308] [LN:D90710] [AC:D90710:AB001340] [PN:Hypothetical protein HI1730] [OR:Escherichia coli] [SR:Escherichia coli(strain:K12) DNA, clone:Kohara clone #175] [DB:genpept-bct1] [DE:Escherichia coli genomic DNA. (15.9 - 16.3 min).] [NT:ORF\_ID:o175#7; similar to PIR Accession Number] [LE:6967] [RE:7899] [DI:direct] >gp:[GI:g1786930] [LN:AE000174] [AC:AE000174:U00096] [PN:putative carboxylase] [GN:ybgK] [FN:putative enzyme; Not classified] [OR:Escherichia coli] [DB:genpept-bct2] [DE:Escherichia coli K-12 MG1655 section 64 of 400 of the complete genome.] [NT:o310; This 310 aa ORF is 48 pct identical (1 gap)] [LE:10112] [RE:11044] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_47763_f3_814	3631	7403	186	61		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_4804643_f1_90	3632	7404	246	81	75	0.0026

Description

gp: [GI:e1332553:g3764009] [LN:PFMAL3P4] [AC:AL008970] [GN:MAL3P4.11] [OR:Plasmodium falciparum] [SR:malaria parasite P. falciparum] [DB:genpept-inv1] [DE:Plasmodium falciparum MAL3P4, complete sequence.] [NT:predicted using hexExon; MAL3P4.11 (PFC0510w),] [LE:68636] [RE:71146] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_4806575_c2_1171	3633	7405	651	216	503	3.7e-48

Description

pir: [LN:H69854] [AC:H69854] [PN:hypothetical protein ykaA] [GN:ykaA] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1181486:g2632006] [LN:BSAJ2571] [AC:AJ002571] [PN:YkaA] [GN:ykaA] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis 168 56 kb DNA fragment between xlyA and ykoR.] [LE:2613] [RE:3230] [DI:complement] >gp: [GI:e1183305:g2633639] [LN:BSUB0007] [AC:Z99110:AL009126] [GN:ykaA] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.] [LE:155562] [RE:156179] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_4876077_f3_796	3634	7406	714	237	778	2.7e-77

Description

pir: [LN:C69868] [AC:C69868] [PN:coenzyme PQQ synthesis homolog ykvL] [GN:ykvL] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1184964:g2633745] [LN:BSUB0008] [AC:Z99111:AL009126] [GN:ykvL] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.] [NT:similar to coenzyme PQQ synthesis] [LE:45218] [RE:45949] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_4885876_c1_1071	3635	7407	918	305	829	1.1e-82

Description

sp: [LN:YVCJ\_BACSU] [AC:006973] [GN:YVCJ] [OR:BACILLUS SUBTILIS] [DE:HYPOTHETICAL 33.9 KD PROTEIN IN CRH-TRXB INTERGENIC REGION] [SP:006973] [DB:swissprot] >pir: [LN:H70031] [AC:H70031] [PN:conserved hypothetical protein yvcJ] [GN:yvcJ] [CL:Bacillus subtilis conserved hypothetical protein yvcJ] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1186165:g2635990] [LN:BSUB0018] [AC:Z99121:AL009126] [GN:yvcJ] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.] [NT:similar to hypothetical proteins] [SP:006973] [LE:171011] [RE:171898] [DI:complement] >gp: [GI:e313026:g1945650] [LN:BSZ94043] [AC:Z94043] [PN:hypothetical protein] [GN:yvcJ] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B. subtilis genomic DNA fragment (88 kb).] [NT:similar to hypothetical MTCY21B4] [SP:006973] [LE:9773] [RE:10660] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_4892878_c3_1357	3636	7408	1077	358	455	4.5e-43

Description

gp: [GI:g1913906] [LN:SAU91741] [AC:U91741] [PN:TagX] [GN:tagX] [FN:teichoic acid biosynthesis] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:Staphylococcus aureus teichoic acid biosynthesis TagB gene, partialcds and TagX and TagD genes, complete cds.] [LE:632] [RE:1471] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_4898376_f2_574	3637	7409	207	68	52	0.024

Description

gp: [GI:g4588017] [LN:AF087657] [AC:AF087657] [PN:NADH-ubiquinone oxidoreductase chain 6] [GN:ND6] [OR:Mitochondrion Agrocybe aegerita] [SR:Agrocybe aegerita] [DB:genpept-pln2] [DE:Agrocybe aegerita NADH-ubiquinone oxidoreductase chain 6 (ND6) gene, mitochondrial gene encoding mitochondrial protein, completecds.] [NT:NADH dehydrogenase] [LE:34] [RE:453] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_5084652_f3_849	3638	7410	507	168	536	1.2e-51

Description

gp: [GI:g1575061] [LN:SAU57060] [AC:U57060] [PN:ScdA] [GN:scdA] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:Staphylococcus aureus scdA gene, complete cds.] [NT:S. aureus cells containing a scdA disruption have] [LE:361] [RE:1035] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_5117793_c3_1531	3639	7411	273	91	197	9.9e-16

Description

sp: [LN:YRN3\_VIBPA] [AC:P46231] [OR:VIBRIO PARAHAEMOLYTICUS] [DE:HYPOTHETICAL PROTEIN IN RNT 5'REGION (ORF3) (FRAGMENT)] [SP:P46231] [DB:swissprot] >gp: [GI:g497126] [LN:VPU06949] [AC:U06949] [PN:ORF3] [OR:Vibrio parahaemolyticus] [DB:genpept-bct1] [DE:Vibrio parahaemolyticus BB22 RNase T (rnt) gene and flagellar motorcomponent (motY) gene, complete cds.] [LE:<1] [RE:420] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_5131265_c2_1243	3640	7412	276	91	80	0.0071

Description

gp: [GI:g3582235] [LN:AE001272] [AC:AE001272] [PN:L. lactis predicted coding region ORF00014] [GN:ORF00014] [OR:Lactococcus lactis] [DB:genpept-bct2] [DE:Lactococcus lactis DPC3147 plasmid pMRC01, complete plasmidsequence.] [NT:hypothetical protein; identified by GeneMark;] [LE:10983] [RE:11600] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_5182962_f1_196	3641	7413	1068	355	295	1.3e-30

Description

sp: [LN:RESE\_BACSU] [AC:P35164] [GN:RESE] [OR:BACILLUS SUBTILIS] [EC:2.7.3.-] [DE:SENSOR PROTEIN RESE,] [SP:P35164] [DB:swissprot] >pir: [LN:H69691] [AC:H69691:S45560] [PN:two-component sensor histidine kinase resE] [GN:resE] [CL:sensor histidine kinase homology] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:g410142] [LN:BACDIA] [AC:L09228] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain 168, sub\_species Marburg) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis spoVA to serA region.] [NT:ORFX18] [LE:22425] [RE:24194] [DI:direct] >gp: [GI:e1185580:g2634746] [LN:BSUB0013] [AC:Z99116:AL009126] [PN:two-component sensor histidine kinase] [GN:resE] [FN:involved in global regulation of aerobic and] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.] [NT:alternate gene name: ypxE] [SP:P35164] [LE:19389] [RE:21158] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503001001_5195393_c3_1352	3642	7414	654	217	1088	3.8e-110
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Description

gp: [GI:e255543:g1617434] [LN:SESIRR] [AC:X99128] [PN:putative iron dependant repressor] [GN:sirR] [OR:Staphylococcus epidermidis] [DB:genpept-bct1] [DE:S.epidermidis sirR gene.] [LE:14] [RE:658] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503001001_5276677_c1_1026	3643	7415	1566	521	703	2.4e-69
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Description

pir: [LN:B64622] [AC:B64622] [PN:osmoprotection protein] [OR:Helicobacter pylori] [DB:pir2] >gp: [GI:g2313949] [LN:AE000593] [AC:AE000593:AE000511] [PN:osmoprotection protein (proWX)] [GN:HP0818] [OR:Helicobacter pylori 26695] [DB:genpept-bct2] [DE:Helicobacter pylori 26695 section 71 of 134 of the complete genome.] [NT:similar to PID:1109685 SP:Q45461 GB:AL009126] [LE:4862] [RE:6523] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503001001_5283592_f1_215	3644	7416	288	95	73	0.014
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Description

gp: [GI:g1054677] [LN:CCCOX3] [AC:X92734] [PN:cytochrome oxidase] [GN:coxIII] [OR:Mitochondrion Chara corallina] [SR:Chara corallina] [DB:genpept-pln1] [DE:C.corallina mitochondrial cox3 gene.] [NT:subunit III] [LE:<1] [RE:>381] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503001001_5292175_c3_1484	3645	7417	1323	440	2112	1.2e-218
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Description

gp: [GI:g3152725] [LN:AF065394] [AC:AF065394] [PN:enolase] [GN:eno] [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus enolase (eno) gene, complete cds.] [NT:ENO; laminin binding protein] [LE:103] [RE:1407] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503001001_53552_f2_450	3646	7418	660	219	179	8.0e-14
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Description

sp: [LN:GRPB\_BACFI] [AC:Q45133] [GN:GRPB] [OR:BACILLUS FIRMUS] [DE:GLUTAMATE-RICH PROTEIN GRPB] [SP:Q45133] [DB:swissprot] >gp: [GI:g1209681] [LN:BFU39410] [AC:U39410] [PN:glutamate-rich protein] [GN:grpB] [OR:Bacillus firmus] [SR:Bacillus firmus strain=OF4] [DB:genpept-bct1] [DE:Bacillus firmus OrfA, OrfB, glutamate-rich protein (grpA), OrfC, and glutamate-rich protein (grpB) genes, complete cds.] [LE:2695] [RE:3219] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_5355325_c3_1454	3647	7419	888	295	526	1.4e-50

Description

sp: [LN:DEGV\_BACSU] [AC:P32436] [GN:DEGV] [OR:BACILLUS SUBTILIS] [DE:DEGV PROTEIN] [SP:P32436] [DB:swissprot] >pir: [LN:D30191] [AC:I40386:D30191:A70042:S28596] [PN:conserved hypothetical protein yviA] [GN:yviA] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:g39848] [LN:BSCOMFG] [AC:Z18629] [PN:U3] [GN:degUorf3] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis comF gene.] [SP:P32436] [LE:1] [RE:846] [DI:direct] >gp: [GI:e1184454:g2636074] [LN:BSUB0019] [AC:Z99122:AL009126] [GN:yviA] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091 to 3809700.] [NT:alternate gene name: degV, sacU; similar to] [LE:45634] [RE:46479] [DI:complement] >gp: [GI:g1762331] [LN:BSU56901] [AC:U56901] [GN:degV] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis putative transcriptional regulator (yvhJ), Ycr59c/YigZ homolog (yvhK), histidine kinase (degS), transcriptional regulator of degradation enzyme (degU), (degV), (comFA), (comFB), (comFC), flagellar protein (yviB), negative regulator of flagellin(flgM), flagellar protein (yviC), flagellar-hook associated protein1 (flgK), flagellar-hook associated protein 3 (flgL), (yviE), transmembrane protein (yviF), (csrA), flagellin (hag), flagellar protein (yviH), flagellar hook-associated protein 2 (fliD), flagellar protein (fliS), flagellar protein (fliT), sigma-54modulator homolog (yviI), and (secA) genes, complete cds.] [LE:4114] [RE:4959] [DI:direct] >gp: [GI:e1184454:g2636074] [LN:BSUB0019] [AC:Z99122:AL009126] [GN:yviA] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept] [DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091 to 3809700.] [NT:alternate gene name: degV, sacU; similar to] [SP:P32436] [LE:45634] [RE:46479] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_5367843_c3_1488	3648	7420	759	252	791	1.1e-78

Description

sp: [LN:EST\_BACST] [AC:Q06174] [GN:EST] [OR:BACILLUS STEAROTHERMOPHILUS] [EC:3.1.1.1] [DE:CARBOXYLESTERASE PRECURSOR,] [SP:Q06174] [DB:swissprot] >pir: [LN:JC1374] [AC:JC1374] [PN:carboxylesterase,] [GN:Est] [OR:Bacillus stearothermophilus] [EC:3.1.1.1] [DB:pir2] >gp: [GI:d1002674:g216314] [LN:BACPBH7] [AC:D12681] [PN:esterase] [OR:Bacillus stearothermophilus] [SR:Bacillus stearothermophilus DNA, clone pBH7] [DB:genpept-bct1] [DE:Bacillus stearothermophilus esterase gene.] [LE:181] [RE:924] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_57800_c3_1494	3649	7421	147	48		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_5869433_f2_542	3650	7422	129	42		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503001001_5869702_f2_595	3651	7423	309	102	87	0.015
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Description

sp: [LN:YMW6\_YEAST] [AC:Q04264:Q04780] [GN:YMR076C:YM9582.01C:YM9916.15C]  
 [OR:SACCHAROMYCES CEREVIAE] [SR:, BAKER'S YEAST] [DE:HYPOTHETICAL 147.0 KD PROTEIN IN ABF2-CHL12 INTERGENIC REGION] [SP:Q04264:Q04780] [DB:swissprot] >pir: [LN:S54451] [AC:S54451:S52836] [PN:hypothetical protein YMR076c:hypothetical protein YM9582.01c:hypothetical protein YM9916.15c] [GN:PDS5] [OR:Saccharomyces cerevisiae] [DB:pir2] [MP:13R]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503001001_5938762_c1_987	3652	7424	1704	567	566	7.8e-55
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Description

sp: [LN:CYDD\_HAEIN] [AC:P45082] [GN:CYDD:HI1157] [OR:HAEMOPHILUS INFLUENZAE] [DE:TRANSPORT ATP-BINDING PROTEIN CYDD] [SP:P45082] [DB:swissprot] >pir: [LN:F64186] [AC:F64186] [PN:ABC-type transport protein cydD] [GN:cydD] [CL:unassigned ATP-binding cassette proteins: ATP-binding cassette homology] [OR:Haemophilus influenzae] [DB:pir2] >gp: [GI:g1574714] [LN:U32795] [AC:U32795:L42023] [PN:ATP-binding protein protein (cydD)] [GN:HI1157] [OR:Haemophilus influenzae Rd] [DB:genpept-bct2] [DE:Haemophilus influenzae Rd section 110 of 163 of the completest genome.] [NT:similar to GB:L21749 SP:P29018 GB:L25859 PID:146416] [LE:6353] [RE:8113] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503001001_6023915_c2_1313	3653	7425	969	322	1144	4.4e-116
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Description

pir: [LN:D70023] [AC:D70023] [PN:lipoic acid synthetase, yutB] [GN:yutB] [CL:lipoic acid synthetase] [OR:Bacillus subtilis] [EC:2.8.1.-] [DB:pir2] >gp: [GI:e1184312:g2635730] [LN:BSUB0017] [AC:Z99120:AL009126] [GN:yutB] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 17 of 21): from 3197001 to 3414420.] [NT:similar to lipoic acid synthetase] [LE:122382] [RE:123188] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503001001_6037756_f3_682	3654	7426	150	49		
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503001001_6050010_f1_177	3655	7427	132	43		
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503001001_6051500_c1_972	3656	7428	189	62		
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_6051537_c1_1063	3657	7429	276	91	112	1.0e-06

Description

sp: [LN:CSBA\_BACSU] [AC:P37953] [GN:CSBA] [OR:BACILLUS SUBTILIS] [DE:CSBA PROTEIN] [SP:P37953] [DB:swissprot] >gp: [GI:g142780] [LN:BACCSBA] [AC:M80473] [GN:csbA] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain 168, sub\_species Marburg) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis csbA and uvr/dinA genes, complete cds.] [NT:putative membrane protein; putative] [LE:380] [RE:610] [DI:direct] >gp: [GI:g142842] [LN:BACDINA76] [AC:M64048] [PN:DNase inhibitor] [GN:dinA] [OR:Bacillus subtilis] [SR:Bacillus subtilis DNA] [DB:genpept-bct1] [DE:Bacillus subtilis DNase inhibitor (dinA76) gene, complete cds and promoter region.] [LE:64] [RE:294] [DI:direct] >gp: [GI:e1184424:g2636044] [LN:BSUB0019] [AC:Z99122:AL009126] [PN:putative membrane protein] [GN:csbA] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091 to 3809700.] [SP:P37953] [LE:17086] [RE:17316] [DI:complement] >gp: [GI:g2618840] [LN:AF017113] [AC:AF017113] [PN:CsbA] [GN:csbA] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis 300-304 degree genomic sequence.] [LE:12977] [RE:13207] [DI:direct] >gp: [GI:e1184424:g2636044] [LN:BSUB0019] [AC:Z99122:AL009126] [PN:putative membrane protein] [GN:csbA] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept] [DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091 to 3809700.] [SP:P37953] [LE:17086] [RE:17316] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_6053176_f1_195	3658	7430	519	172		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_6056628_c3_1339	3659	7431	150	49		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_6057338_c3_1518	3660	7432	840	279	622	9.1e-61

Description

pir: [LN:H70015] [AC:H70015] [PN:hypothetical protein yunE] [GN:yunE] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1184317:g2635735] [LN:BSUB0017] [AC:Z99120:AL009126] [GN:yunE] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 17 of 21): from 3197001 to 3414420.] [LE:127136] [RE:127957] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_6094177_c2_1235	3661	7433	123	40		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_6101581_f1_74	3662	7434	180	59		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_6257763_c3_1479	3663	7435	660	219	189	1.7e-13

Description

gp: [GI:g2246532] [LN:U93872] [AC:U93872] [OR:Kaposi's sarcoma-associated herpesvirus] [SR:Kaposi's sarcoma-associated herpesvirus - Human herpesvirus 8] [DB:genpept-vrl] [DE:Kaposi's sarcoma-associated herpesvirus glycoprotein M, DNAreplication protein, glycoprotein, DNA replication protein, FLICEinhibitory protein and v-cyclin genes, complete cds, and tegumentprotein gene, partial cds.] [NT:ORF 73, contains large complex repeat CR 73] [LE:124324] [RE:127593] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_626592_c1_935	3664	7436	852	283	233	1.5e-19

Description

pir: [LN:A69463] [AC:A69463] [PN:2-hydroxy-6-oxo-6-phenylhexa-2,4-dienoic acid hydrolase (pcbD) homolog] [OR:Archaeoglobus fulgidus] [DB:pir2] >gp: [GI:g2648849] [LN:AE000986] [AC:AE000986:AE000782] [PN:2-hydroxy-6-oxo-6-phenylhexa-2,4-dienoic acid] [GN:AF1706] [OR:Archaeoglobus fulgidus] [DB:genpept-bct2] [DE:Archaeoglobus fulgidus section 121 of 172 of the complete genome.] [NT:similar to GP:1395174 percent identity: 29.41;] [LE:11775] [RE:12491] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_6423376_f3_670	3665	7437	261	86		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_6437525_f3_862	3666	7438	294	97		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_6440640_c3_1379	3667	7439	1278	425	139	6.0e-06

Description

pir: [LN:D71621] [AC:D71621] [PN:hypothetical protein PFB0185w] [GN:PFB0185w] [OR:Plasmodium falciparum] [DB:pir2] >gp: [GI:g3845117] [LN:AE001378] [AC:AE001378:AE001362] [PN:hypothetical protein] [GN:PFB0185w] [OR:Plasmodium falciparum] [SR:malaria parasite P. falciparum] [DB:genpept-inv2] [DE:Plasmodium falciparum chromosome 2, section 15 of 73 of thecomplete sequence.] [NT:predicted by GlimmerM] [LE:6504:8652] [RE:8473:9075] [DI:directJoin]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_6444037_c2_1180	3668	7440	144	47		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_6642827_c3_1342	3669	7441	2403	800	1527	1.1e-156

Description

pir:[LN:A70010] [AC:A70010] [PN:NADH dehydrogenase homolog yufT] [GN:yufT] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1184238:g2635656] [LN:BSUB0017] [AC:Z99120:AL009126] [GN:yufT] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 17 of 21): from 3197001 to 3414420.] [NT:similar to NADH dehydrogenase] [LE:48758] [RE:51082] [DI:direct] >gp:[GI:e311455:g1934817] [LN:BSZ93937] [AC:Z93937] [PN:unknown] [GN:yufT] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B. subtilis genomic DNA fragment from yufK to yufV.] [NT:potential Na/H antiporter/phaA homologue/NADH] [LE:10546] [RE:12870] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_6650312_f2_600	3670	7442	141	46		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_6675016_c1_1077	3671	7443	132	43		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_6680312_f2_518	3672	7444	714	237	211	4.7e-17

Description

gp:[GI:g3329623] [LN:CELF36H12] [AC:AF078790] [GN:F36H12.3] [OR:Caenorhabditis elegans] [DB:genpept-inv2] [DE:Caenorhabditis elegans cosmid F36H12.] [NT:coded for by C. elegans cDNA CEMSF30F] [LE:21606:21872:22500:22677] [RE:21701:22454:22629:22875] [DI:directJoin]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_6681577_c1_1110	3673	7445	432	143	277	3.3e-24

Description

pir:[LN:G70020] [AC:G70020] [PN:hypothetical protein yusF] [GN:yusF] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1184356:g2635774] [LN:BSUB0017] [AC:Z99120:AL009126] [GN:yusF] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 17 of 21): from 3197001 to 3414420.] [LE:167450] [RE:167890] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_6695968_c2_1320	3674	7446	1470	489	2005	2.5e-207

Description

gp:[GI:g4530241] [LN:AF101234] [AC:AF101234] [PN:D-alanine-D-alanyl carrier protein ligase DltA] [GN:dltA] [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus dltABCD operon, complete sequence; and unknown gene.] [LE:1590] [RE:3047] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_6822175_c2_1222	3675	7447	1914	637	1229	4.3e-125

Description

pir:[LN:F69901] [AC:F69901] [PN:DNA helicase recQ:ATP-dependent DNA helicase homolog yocI] [GN:yocI] [CL:recQ protein:DEAD/H box helicase homology:recQ helicase homology] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:g2619051] [LN:AF027868] [AC:AF027868] [PN:RecQ homolog] [GN:yocI] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis chromosome region between terC and odhAB.] [NT:similar to E.coli RecQ protein (607 aa)] [LE:74004] [RE:75779] [DI:complement] >gp:[GI:e1185394:g2634315] [LN:BSUB0011] [AC:Z99114:AL009126] [GN:yocI] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.] [NT:similar to ATP-dependent DNA helicase] [LE:93095] [RE:94870] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503001001_6823453_c3_1346	3676	7448	483	160	270	1.8e-23
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Description

gp:[GI:d1036085:g4001729] [LN:AB015981] [AC:AB015981] [PN:MnhE] [GN:mnhE] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus (strain:209P) DNA] [DB:genpept-bct1] [DE:Staphylococcus aureus genes for OrfA, MnhA, MnhB, MnhC, MnhD, MnhE, MnhF and MnhG, complete cds.] [LE:5474] [RE:5953] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503001001_6829638_c3_1402	3677	7449	186	61		
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503001001_6833313_c3_1371	3678	7450	1920	639	550	3.9e-53
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Description

pir:[LN:B70001] [AC:B70001] [PN:ABC transporter (permease) homolog ytsD] [GN:ytsD] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1185910:g2635521] [LN:BSUB0016] [AC:Z99119:AL009126] [GN:ytsD] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.] [NT:similar to ABC transporter (permease)] [LE:110708] [RE:112648] [DI:complement] >gp:[GI:g2293178] [LN:AF008220] [AC:AF008220] [PN:YtsD] [GN:ytsD] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis rRNA-dnaB genomic region.] [NT:similarity to NADH dehydrogenase] [LE:67779] [RE:69719] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503001001_6836088_c1_1118	3679	7451	1320	439	1260	2.2e-128
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Description

pir:[LN:G70019] [AC:G70019] [PN:conserved hypothetical protein yurX] [GN:yurX] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1184348:g2635766] [LN:BSUB0017] [AC:Z99120:AL009126] [GN:yurX] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.] [NT:similar to hypothetical proteins] [LE:160723] [RE:162036] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_6929512_c1_1119	3680	7452	1416	471	2098	3.6e-217

Description

pir:[LN:D70019] [AC:D70019] [PN:conserved hypothetical protein yurU] [GN:yurU] [CL: Methanobacterium thermoautotrophicum ABC transporter chain Ycf24] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1184345:g2635763] [LN:BSUB0017] [AC:Z99120:AL009126] [GN:yurU] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 17 of 21): from 3197001 to 3414420.] [NT:similar to hypothetical proteins] [LE:157652] [RE:159049] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_7042878_f1_40	3681	7453	177	58		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_7239188_f2_519	3682	7454	675	224	491	6.9e-47

Description

pir:[LN:D70033] [AC:D70033] [PN:conserved hypothetical protein yvdD] [GN:yvdD] [CL:yeast conserved hypothetical protein YJL055w] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1186152:g2635977] [LN:BSUB0018] [AC:Z99121:AL009126] [GN:yvdD] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 18 of 21): from 3399551 to 3609060.] [NT:similar to hypothetical proteins] [LE:158450] [RE:159025] [DI:complement] >gp:[GI:e313036:g1945663] [LN:BSZ94043] [AC:Z94043] [PN:hypothetical protein] [GN:yvdD] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B. subtilis genomic DNA fragment (88 kb).] [NT:similar to YJF5\_YEAST hypothetical 26.9 kd protein] [LE:22646] [RE:23221] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_7800_c1_1093	3683	7455	198	65	54	0.033

Description

gp:[GI:g3789915] [LN:AF083442] [AC:AF083442] [PN:G protein-coupled receptor G2A] [OR:Mus musculus] [SR:house mouse] [DB:genpept-rod] [DE:Mus musculus G protein-coupled receptor G2A mRNA, complete cds.] [LE:147] [RE:1295] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_781415_c3_1393	3684	7456	165	54		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_783375_c2_1236	3685	7457	180	59		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_788950_c3_1347	3686	7458	531	176	219	4.6e-18

Description

pir:[LN:E70008] [AC:E70008] [PN:conserved hypothetical protein yufB] [GN:yufB] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1184243:g2635661] [LN:BSUB0017] [AC:Z99120:AL009126] [GN:yufB] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 17 of 21): from 3197001 to 3414420.] [NT:similar to hypothetical proteins] [LE:54068] [RE:54442] [DI:direct] >gp:[GI:e311512:g1934774] [LN:BSZ93932] [AC:Z93932] [PN:unknown] [GN:yufB] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B. subtilis genomic DNA fragment from yufA to yufE.] [LE:7086] [RE:7460] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_821963_c2_1165	3687	7459	546	181	103	0.0018

Description

gp:[GI:g4731376] [LN:AF135127] [AC:AF135127:AF047896] [PN:isoflavone reductase homolog Bet v 5] [GN:BETV5] [OR:Betula pendula] [SR:European white birch] [DB:genpept-pln2] [DE:Betula pendula isoflavone reductase homolog Bet v 5 (BETV5) mRNA, partial cds.] [NT:allergen; IgE binding protein] [LE:1] [RE:>900] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_822777_c3_1397	3688	7460	159	52		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_870300_c1_958	3689	7461	153	50		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_899177_c3_1335	3690	7462	930	309	596	5.2e-58

Description

pir:[LN:G70046] [AC:G70046] [PN:iron-binding protein homolog yvrC] [GN:yvrC] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1249807:g2832811] [LN:BS43KBDNA] [AC:AJ223978] [PN:putative metal binding protein, YvrC] [GN:yvrC] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis 42.7kB DNA fragment from yvsA to yvqA.] [LE:23792] [RE:24736] [DI:direct] >gp:[GI:e1184397:g2635815] [LN:BSUB0017] [AC:Z99120:AL009126] [GN:yvrC] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 17 of 21): from 3197001 to 3414420.] [NT:similar to iron-binding protein] [LE:205551] [RE:206495] [DI:complement] >gp:[GI:e1186006:g2635831] [LN:BSUB0018] [AC:Z99121:AL009126] [GN:yvrC] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 18 of 21): from 3399551 to 3609060.] [NT:similar to iron-binding protein] [LE:3001] [RE:3945] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_900256_c1_1017	3691	7463	210	69		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_959437_c1_965	3692	7464	159	52		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_9642_f1_227	3693	7465	876	291	769	2.4e-76

Description

pir:[LN:E70006] [AC:E70006] [PN:probable bacitracin resistance protein (undecapreno) yubB] [GN:yubB] [CL:Escherichia coli bacitracin resistance protein bacA] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1185988:g2635599] [LN:BSUB0016] [AC:Z99119:AL009126] [GN:yubB] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 16 of 21): from 2997771 to 3213410.] [NT:similar to bacitracin resistance protein] [LE:195935] [RE:196765] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_969075_c1_1109	3694	7466	354	117	359	6.7e-33

Description

pir:[LN:B70021] [AC:B70021] [PN:arsenate reductase homolog yusI] [GN:yusI] [CL:hypothetical protein yjbD] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1184359:g2635777] [LN:BSUB0017] [AC:Z99120:AL009126] [GN:yusI] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 17 of 21): from 3197001 to 3414420.] [NT:similar to arsenate reductase] [LE:168632] [RE:168988] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_969555_f1_218	3695	7467	168	55		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_969812_f1_63	3696	7468	123	40		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_970327_c2_1301	3697	7469	297	98	167	1.5e-12

Description

pir:[LN:F70020] [AC:F70020] [PN:thioredoxin homolog yusE] [GN:yusE] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1184355:g2635773] [LN:BSUB0017] [AC:Z99120:AL009126] [GN:yusE] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 17 of 21): from 3197001 to 3414420.] [NT:similar to thioredoxin] [LE:167128] [RE:167448] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503001001_973400_f3_690	3698	7470	180	59	43	0.013

Description

gp:[GI:e1363550:g4127809] [LN:EFAJ3161] [AC:AJ223161] [PN:hypothetical protein] [GN:orf6] [OR:Enterococcus faecalis] [DB:genpept-bct1] [DE:Enterococcus faecalis plasmid pS86, rep86 and mob86 genes.] [LE:4421] [RE:4732] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_978426_c1_1043	3699	7471	978	325	1338	1.2e-136

Description

gp: [GI:e1330452:g3724155] [LN:SAA005352] [AC:AJ005352] [PN:membrane protein] [GN:sstA] [FN:iron transport protein] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:Staphylococcus aureus, Sst putative iron transport operon.] [LE:273] [RE:1245] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_9882950_c2_1204	3700	7472	1350	449	1090	2.3e-110

Description

sp: [LN:YHDP\_BACSU] [AC:007585] [GN:YHDP] [OR:BACILLUS SUBTILIS] [DE:HYPOTHETICAL 49.9 KD PROTEIN IN CITA-SSPB INTERGENIC REGION] [SP:007585] [DB:swissprot] >pir: [LN:F69826] [AC:F69826] [PN:hemolysin homolog yhdP] [GN:yhdP] [CL:hypothetical protein HI0107] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1182956:g2633290] [LN:BSUB0006] [AC:Z99109:AL009126] [GN:yhdP] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 6 of 21): from 999501 to 1209940.] [NT:similar to hemolysin] [SP:007585] [LE:32043] [RE:33377] [DI:complement] >gp: [GI:e1191881:g2226211] [LN:BSY14082] [AC:Y14082] [PN:hypothetical protein] [GN:yhdP] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis chromosomal DNA, region 72 to 75 degrees: spoVRto sspB.] [NT:Similarity to yhdT, this submission, and to] [SP:007585] [LE:18691] [RE:20025] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_9884625_f2_464	3701	7473	1509	502	1226	9.0e-125

Description

sp: [LN:YCLF\_BACSU] [AC:P94408] [GN:YCLF] [OR:BACILLUS SUBTILIS] [DE:HYPOTHETICAL 53.3 KD PROTEIN IN SFP-GERKA INTERGENIC REGION] [SP:P94408] [DB:swissprot] >pir: [LN:C69762] [AC:C69762] [PN:di-tripeptide ABC transporter (membrane pr) homolog yclf] [GN:yclf] [CL:peptide transporter protein] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1182334:g2632668] [LN:BSUB0003] [AC:Z99106:AL009126] [GN:yclf] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 3 of 21): from 402751 to 611850.] [NT:similar to di-tripeptide ABC transporter (membrane) [SP:P94408] [LE:13065] [RE:14543] [DI:complement] >gp: [GI:d1009635:g1805438] [LN:D50453] [AC:D50453] [PN:homologue of Di-tripeptide transporter Dtp of L.] [GN:yclf] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:168 trpC2) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis DNA for 25-36 degree region containing theamyE-srfA region, complete cds.] [LE:95468] [RE:96946] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503001001_989010_c1_1128	3702	7474	408	135	371	3.6e-34

Description

pir: [LN:G70024] [AC:G70024] [PN:conserved hypothetical protein yutM] [GN:yutM] [CL:conserved hypothetical protein HI0376] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1184295:g2635713] [LN:BSUB0017] [AC:Z99120:AL009126] [GN:yutM] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 17 of 21): from 3197001 to 3414420.] [NT:similar to hypothetical proteins] [LE:107656] [RE:108018] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503012391_11291_c2_183	3703	7475	153	50		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503012391_1369012_c2_207	3704	7476	126	41		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503012391_13790943_c1_161	3705	7477	1644	547	2797	3.0e-291

Description

pir:[LN:C56976] [AC:C56976] [PN:transfer complex protein TrsK] [GN:trsK] [OR:Staphylococcus aureus] [DB:pir2] >gp:[GI:g310618] [LN:STATRSC] [AC:L11998] [GN:trsK] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus (individual\_isolate pG01) DNA] [DB:genpept-bct1] [DE:Staphylococcus aureus conjugative transfer gene complex (trs).] [NT:putative] [LE:10475] [RE:12115] [DI:direct] >gp:[GI:g3676445] [LN:AF051917] [AC:AF051917:L19570] [PN:putative membrane protein TraK] [GN:traK] [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus plasmid pSK41, complete sequence.] [NT:similar to transfer-associated proteins of] [LE:34078] [RE:35718] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503012391_14507827_c3_220	3706	7478	168	55	273	8.7e-24

Description

pir:[LN:F56976] [AC:F56976] [PN:transfer complex protein TrsO'] [OR:Staphylococcus aureus] [DB:pir2] >gp:[GI:g3676448] [LN:AF051917] [AC:AF051917:L19570] [PN:unknown] [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus plasmid pSK41, complete sequence.] [NT:Orf55; possibly truncated by IS257 transposon] [LE:37179] [RE:37346] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503012391_14844187_c2_195	3707	7479	3081	1026	5411	0.0

Description

sp:[LN:SYIP\_STAAU] [AC:P41368] [GN:MUPR] [OR:STAPHYLOCOCCUS AUREUS] [EC:6.1.1.5] [DE:(ISOLEUCINE--TRNA LIGASE) (ILERS) (MUPIROCIN RESISTANCE PROTEIN)] [SP:P41368] [DB:swissprot] >gp:[GI:g581558] [LN:SADNAMUPR] [AC:X75439] [PN:isoleucyl tRNA synthetase] [GN:ileS] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:S.aureus plasmid encoded DNA, mup R gene.] [SP:P41368] [LE:477] [RE:3551] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503012391_15631901_c3_234	3708	7480	645	214	943	8.8e-95

Description

gp:[GI:g3676416] [LN:AF051917] [AC:AF051917:L19570] [PN:putative resolvase Res] [GN:res] [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus plasmid pSK41, complete sequence.] [LE:2779] [RE:3336] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503012391_156910_f2_62	3709	7481	483	160	729	4.2e-72

Description

gp:[GI:g3676415] [LN:AF051917] [AC:AF051917:L19570] [PN:unknown] [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus plasmid pSK41, complete sequence.] [NT:Orf149] [LE:2068] [RE:2484] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503012391_19625062_c3_225	3710	7482	165	54		
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503012391_19665885_c1_175	3711	7483	1728	575	2999	0.0
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Description

gp: [GI:g3676419] [LN:AF051917] [AC:AF051917:L19570] [PN:LtrC-like protein]  
 [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus plasmid pSK41,  
 complete sequence.] [NT:Orf575; similar to Lactococcus lactis pRS01 LtrC] [LE:6350]  
 [RE:8074] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503012391_19744010_c3_232	3712	7484	288	95	466	3.1e-44
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Description

gp: [GI:g3676414] [LN:AF051917] [AC:AF051917:L19570] [PN:unknown] [OR:Staphylococcus  
 aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus plasmid pSK41, complete sequence.]  
 [NT:Orf423] [LE:755] [RE:2026] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503012391_2115625_f2_61	3713	7485	195	64		
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503012391_2150037_c1_180	3714	7486	336	111	464	5.0e-44
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Description

gp: [GI:g3676421] [LN:AF051917] [AC:AF051917:L19570] [PN:unknown] [OR:Staphylococcus  
 aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus plasmid pSK41, complete sequence.]  
 [NT:Orf90] [LE:10316] [RE:10588] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503012391_21754035_f3_110	3715	7487	141	46		
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503012391_23468753_c3_236	3716	7488	1647	548	2838	1.4e-295
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Description

gp: [GI:g3676418] [LN:AF051917] [AC:AF051917:L19570] [PN:unknown] [OR:Staphylococcus  
 aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus plasmid pSK41, complete sequence.]  
 [NT:Orf538] [LE:4531] [RE:6147] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503012391_23594712_c2_211	3717	7489	309	102	392	2.1e-36

Description

gp: [GI:g3676422] [LN:AF051917] [AC:AF051917:L19570] [PN:putative membrane protein] [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus plasmid pSK41, complete sequence.] [NT:Orf77] [LE:10692] [RE:10925] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503012391_23603382_c2_196	3718	7490	603	200	688	9.2e-68

Description

sp: [LN:YIL2\_STAAU] [AC:P41370] [OR:STAPHYLOCOCCUS AUREUS] [DE:HYPOTHETICAL PROTEIN IN ILES 3'REGION (ORF C) (FRAGMENT)] [SP:P41370] [DB:swissprot] >pir: [LN:S40262] [AC:S40262] [PN:hypothetical protein C] [OR:Staphylococcus aureus] [DB:pir2] >gp: [GI:g438228] [LN:SADNAMUPR] [AC:X75439] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:S.aureus plasmid encoded DNA, mup R gene.] [NT:ORF C] [SP:P41370] [LE:3621] [RE:>4013] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503012391_23651712_c2_191	3719	7491	480	159	779	2.1e-77

Description

pir: [LN:B56976] [AC:B56976] [PN:transfer protein complex TrsJ] [GN:trsJ] [OR:Staphylococcus aureus] [DB:pir2] >gp: [GI:g310617] [LN:STATRSC] [AC:L11998] [GN:trsJ] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus (individual\_isolate pG01) DNA] [DB:genpept-bct1] [DE:Staphylococcus aureus conjugative transfer gene complex (trs).] [NT:putative] [LE:10014] [RE:10478] [DI:direct] >gp: [GI:g3676444] [LN:AF051917] [AC:AF051917:L19570] [PN:putative membrane protein TraJ] [GN:traJ] [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus plasmid pSK41, complete sequence.] [LE:33617] [RE:34081] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503012391_23727302_c3_215	3720	7492	1296	431	2175	2.5e-225

Description

pir: [LN:G36891] [AC:G36891] [PN:transfer complex protein TrsF] [GN:trsF] [OR:Staphylococcus aureus] [DB:pir2] >gp: [GI:g310613] [LN:STATRSC] [AC:L11998] [GN:trsF] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus (individual\_isolate pG01) DNA] [DB:genpept-bct1] [DE:Staphylococcus aureus conjugative transfer gene complex (trs).] [NT:putative] [LE:5011] [RE:6291] [DI:direct] >gp: [GI:g3676440] [LN:AF051917] [AC:AF051917:L19570] [PN:putative membrane protein TraF] [GN:traF] [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus plasmid pSK41, complete sequence.] [LE:28614] [RE:29894] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503012391_23959802_c2_201	3721	7493	234	77		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503012391_23959802_f1_16	3722	7494	162	53		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503012391_23959802_f1_32	3723	7495	135	44		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503012391_23959802_f1_51	3724	7496	123	40		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503012391_23959802_f2_70	3725	7497	174	57		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503012391_23959802_f3_119	3726	7498	123	40		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503012391_24001537_c2_187	3727	7499	750	249	1184	2.5e-120

Description

pir:[LN:E36891] [AC:E36891] [PN:transfer complex protein TrsD] [GN:trsD]  
 [OR:Staphylococcus aureus] [DB:pir2] >gp:[GI:g310611] [LN:STATRSC] [AC:L11998]  
 [GN:trsD] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus (individual\_isolate  
 pG01) DNA] [DB:genpept-bct1] [DE:Staphylococcus aureus conjugative transfer gene  
 complex (trs).] [NT:putative] [LE:2283] [RE:2966] [DI:direct] >gp:[GI:g3676438]  
 [LN:AF051917] [AC:AF051917:L19570] [PN:TraD] [GN:traD] [OR:Staphylococcus aureus]  
 [DB:genpept-bct2] [DE:Staphylococcus aureus plasmid pSK41, complete séquence.]  
 [LE:25886] [RE:26569] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503012391_24298387_c1_171	3728	7500	147	48	68	0.045

Description

sp:[LN:PSBH\_CHLVU] [AC:P56323] [GN:PSBH] [OR:CHLORELLA VULGARIS] [DE:PHOTOSYSTEM II 10  
 KD PHOSPHOPROTEIN] [SP:P56323] [DB:swissprot]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503012391_24393803_f1_28	3729	7501	171	56		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503012391_24415937_c2_189	3730	7502	489	162	819	1.2e-81

Description

pir: [LN:I36891] [AC:I36891] [PN:transfer complex protein TrsH] [GN:trsH]  
 [OR:Staphylococcus aureus] [DB:pir2] >gp: [GI:g310615] [LN:STATRSC] [AC:L11998]  
 [GN:trsH] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus (individual\_isolate  
 pG01) DNA] [DB:genpept-bct1] [DE:Staphylococcus aureus conjugative transfer gene  
 complex (trs).] [NT:putative] [LE:7395] [RE:7880] [DI:direct] >gp: [GI:g3676442]  
 [LN:AF051917] [AC:AF051917:L19570] [PN:lipoprotein TraH] [GN:traH] [OR:Staphylococcus  
 aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus plasmid pSK41, complete sequence.]  
 [NT:signal peptide recognized as a pheromone by the] [LE:30998] [RE:31483] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503012391_24664812_c1_155	3731	7503	423	140	671	5.8e-66

Description

pir: [LN:D36891] [AC:D36891] [PN:transfer complex protein TrsC] [GN:trsC]  
 [OR:Staphylococcus aureus] [DB:pir2] >gp: [GI:g310610] [LN:STATRSC] [AC:L11998]  
 [GN:trsC] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus (individual\_isolate  
 pG01) DNA] [DB:genpept-bct1] [DE:Staphylococcus aureus conjugative transfer gene  
 complex (trs).] [NT:putative] [LE:1889] [RE:2296] [DI:direct] >gp: [GI:g3676437]  
 [LN:AF051917] [AC:AF051917:L19570] [PN:putative membrane protein TraC] [GN:traC]  
 [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus plasmid pSK41,  
 complete sequence.] [LE:25492] [RE:25899] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503012391_24723137_f1_49	3732	7504	225	74	315	3.1e-28

Description

pir: [LN:A36891] [AC:A36891] [PN:transfer complex protein TrsN] [GN:trsN]  
 [OR:Staphylococcus aureus] [DB:pir2] >gp: [GI:g3676434] [LN:AF051917]  
 [AC:AF051917:L19570] [PN:putative regulator of transfer genes ArtA] [GN:artA]  
 [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus plasmid pSK41,  
 complete sequence.] [LE:23764] [RE:23952] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503012391_24792033_c2_192	3733	7505	138	45		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503012391_25587777_f1_52	3734	7506	264	87	444	6.6e-42

Description

gp: [GI:g3676425] [LN:AF051917] [AC:AF051917:L19570] [PN:unknown] [OR:Staphylococcus  
 aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus plasmid pSK41, complete sequence.]  
 [NT:Orf86] [LE:12564] [RE:12824] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503012391_26594052_c1_150	3735	7507	336	111	567	6.1e-55

Description

gp: [GI:g3676424] [LN:AF051917] [AC:AF051917:L19570] [PN:unknown] [OR:Staphylococcus  
 aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus plasmid pSK41, complete sequence.]  
 [NT:Orf109] [LE:12231] [RE:12560] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503012391_26600927_c2_206	3736	7508	786	261	1347	1.4e-137

Description

gp: [GI:g3676417] [LN:AF051917] [AC:AF051917:L19570] [PN:unknown] [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus plasmid pSK41, complete sequence.] [NT:Orf259] [LE:3618] [RE:4397] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503012391_29558262_c2_205	3737	7509	129	42		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503012391_30273550_c1_162	3738	7510	432	143	671	5.8e-66

Description

pir: [LN:E56976] [AC:E56976] [PN:transfer complex protein TrsM] [GN:trsM] [CL:single-stranded DNA-binding protein homology] [OR:Staphylococcus aureus] [DB:pir2] >gp: [GI:g310620] [LN:STATRSC] [AC:L11998] [GN:trsM] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus (individual\_isolate pG01) DNA] [DB:genpept-bct1] [DE:Staphylococcus aureus conjugative transfer gene complex (trs).] [NT:putative] [LE:13127] [RE:13519] [DI:direct] >gp: [GI:g3676447] [LN:AF051917] [AC:AF051917:L19570] [PN:putative single-stranded DNA binding protein] [GN:traM] [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus plasmid pSK41, complete sequence.] [LE:36730] [RE:37122] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503012391_30503392_c2_188	3739	7511	1083	360	1889	5.0e-195

Description

gp: [GI:g3676441] [LN:AF051917] [AC:AF051917:L19570] [PN:putative membrane protein TraG] [GN:traG] [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus plasmid pSK41, complete sequence.] [LE:29912] [RE:30988] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503012391_33786251_c3_230	3740	7512	1113	370	1926	6.0e-199

Description

sp: [LN:AACA\_STAAU] [AC:P14507] [GN:AACA-APHD] [OR:STAPHYLOCOCCUS AUREUS:ENTEROCOCCUS FAECALIS] [SR:,STREPTOCOCCUS FAECALIS] [EC:2.3.1.-:2.7.1.-] [DE:AMINOGLYCOSIDE PHOSPHOTRANSFERASE, (APH(2'))] [SP:P14507] [DB:swissprot] >pir: [LN:S26353] [AC:S26353] [PN:aminoglycoside resistance protein aacA-aphD] [OR:Staphylococcus aureus] [DB:pir2] >pir: [LN:A26048] [AC:A26048] [PN:aminoglycoside acetyltransferase] [OR:Enterococcus faecalis] [DB:pir2] >gp: [GI:g152948] [LN:STAAGLSRA] [AC:M18086:M29261] [PN:aminoglycoside resistance protein] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus (strain SK982) DNA] [DB:genpept-bct1] [DE:S.aureus transposon 4001 aacA-aphD aminoglycoside resistance gene, complete cds, and right and left IS256 transposase genes.] [LE:1725] [RE:3164] [DI:direct] >gp: [GI:g153586] [LN:STRERP] [AC:M13771] [OR:Enterococcus faecalis] [SR:S.faecalis DNA, clone pSF815A] [DB:genpept-bct1] [DE:Streptococcus faecalis 6'-aminoglycoside acetyltransferasephosphotransferase (AAC(6')-APH(2')) bifunctional resistanceprotein, complete cds.] [NT: AAC(6')-APH(2') bifunctional resistance protein] [LE:304] [RE:1743] [DI:direct] >gp: [GI:g3676454] [LN:AF051917] [AC:AF051917:L19570] [PN:bifunctional aminoglycoside modifying enzyme] [GN:aacA-aphD] [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus plasmid pSK41, complete sequence.] [LE:42505] [RE:43944] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503012391_33786251_f2_66	3741	7513	390	129	644	4.2e-63

Description

sp: [LN:TRA6\_STAAU] [AC:P19775] [GN:TNP] [OR:STAPHYLOCOCCUS AUREUS] [DE:TRANSPOSAE FOR INSERTION SEQUENCE ELEMENT IS256 IN TRANSPOSON TN4001] [SP:P19775] [DB:swissprot] >pir: [LN:JS0296] [AC:JS0296] [PN:transposase] [GN:tnp] [OR:Staphylococcus aureus] [DB:pir2] >gp: [GI:g152947] [LN:STAAGLSRA] [AC:M18086:M29261] [PN:transposase] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus (strain SK982) DNA] [DB:genpept-bct1] [DE:S.aureus transposon 4001 aacA-aphD aminoglycoside resistance gene, complete cds, and right and left IS256 transposase genes.] [LE:102] [RE:1274] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503012391_34242300_c1_158	3742	7514	2037	678	3430	0.0

Description

pir: [LN:F36891] [AC:F36891] [PN:transfer complex protein TrsE] [OR:Staphylococcus aureus] [DB:pir2] >gp: [GI:g310612] [LN:STATRSC] [AC:L11998] [GN:trsE] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus (individual\_isolate pG01) DNA] [DB:genpept-bct1] [DE:Staphylococcus aureus conjugative transfer gene complex (trs).] [NT:putative] [LE:2981] [RE:4999] [DI:direct] >gp: [GI:g3676439] [LN:AF051917] [AC:AF051917:L19570] [PN:putative ATPase TraE] [GN:traE] [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus plasmid pSK41, complete sequence.] [LE:26584] [RE:28602] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503012391_34642562_c1_174	3743	7515	207	68		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503012391_35397177_c2_182	3744	7516	1062	353	1760	2.3e-181

Description

gp: [GI:g3676423] [LN:AF051917] [AC:AF051917:L19570] [PN:unknown] [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus plasmid pSK41, complete sequence.] [NT:Orf346] [LE:11188] [RE:12228] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503012391_35397177_c3_241	3745	7517	132	44	142	3.1e-09

Description

gp: [GI:g3676423] [LN:AF051917] [AC:AF051917:L19570] [PN:unknown] [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus plasmid pSK41, complete sequence.] [NT:Orf346] [LE:11188] [RE:12228] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503012391_36048212_c3_221	3746	7518	774	257	783	7.9e-78

Description

sp: [LN:YIL1\_STAAU] [AC:P41369] [OR:STAPHYLOCOCCUS AUREUS] [DE:HYPOTHETICAL PROTEIN IN IILES 5'REGION (ORF B) (FRAGMENT)] [SP:P41369] [DB:swissprot] >pir: [LN:S40261] [AC:S40261] [PN:hypothetical protein B] [OR:Staphylococcus aureus] [DB:pir2] >gp: [GI:g438227] [LN:SADNAMUPR] [AC:X75439] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:S.aureus plasmid encoded DNA, mup R gene.] [NT:ORF B] [SP:P41369] [LE:<1] [RE:450] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503012391_36605260_c1_169	3747	7519	630	209	1077	5.5e-109
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Description

gp: [GI:g3676413] [LN:AF051917] [AC:AF051917:L19570] [PN:unknown] [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus plasmid pSK41, complete sequence.] [NT:Orf204] [LE:72] [RE:686] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503012391_3907943_f3_103	3748	7520	2010	669	3498	0.0
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Description

gp: [GI:g3676420] [LN:AF051917] [AC:AF051917:L19570] [PN:oriT nickase Nes] [GN:nes] [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus plasmid pSK41, complete sequence.] [LE:8115] [RE:10112] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503012391_3908407_c3_214	3749	7521	123	40		
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503012391_4300002_c1_153	3750	7522	126	41		
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503012391_4428802_f2_57	3751	7523	168	55		
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503012391_4486075_c1_154	3752	7524	975	324	1640	1.2e-168
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Description

pir: [LN:B36891] [AC:B36891] [PN:transfer complex protein TrsA] [GN:trsA] [OR:Staphylococcus aureus] [DB:pir2] >gp: [GI:g310608] [LN:STATRSC] [AC:L11998] [GN:trsA] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus (individual\_isolate pG01) DNA] [DB:genpept-bct1] [DE:Staphylococcus aureus conjugative transfer gene complex (trs).] [NT:putative] [LE:521] [RE:1495] [DI:direct] >gp: [GI:g3676435] [LN:AF051917] [AC:AF051917:L19570] [PN:TraA] [GN:traA] [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus plasmid pSK41, complete sequence.] [LE:24124] [RE:25098] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503012391_4586062_c1_176	3753	7525	141	46		
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AT7503012391_4724035_c1_170	3754	7526	1134	377	1728	5.7e-178

Description

gp: [GI:g3676414] [LN:AF051917] [AC:AF051917:L19570] [PN:unknown] [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus plasmid pSK41, complete sequence.] [NT:Orf423] [LE:755] [RE:2026] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503012391\_4745437\_c2\_190

3755 7527 2118 705 3603 0.0

Description

pir: [LN:A56976] [AC:A56976] [PN:transfer complex protein TrsI] [GN:trsI] [OR:Staphylococcus aureus] [DB:pir2] >gp: [GI:g310616] [LN:STATRSC] [AC:L11998] [GN:trsI] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus (individual\_isolate pG01) DNA] [DB:genpept-bct1] [DE:Staphylococcus aureus conjugative transfer gene complex (trs).] [NT:putative] [LE:7896] [RE:9998] [DI:direct] >gp: [GI:g3676443] [LN:AF051917] [AC:AF051917:L19570] [PN:putative topoisomerase TraI] [GN:traI] [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus plasmid pSK41, complete sequence.] [LE:31499] [RE:33601] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503012391\_5109675\_c2\_186

3756 7528 324 107 535 1.5e-51

Description

pir: [LN:C36891] [AC:C36891] [PN:transfer complex protein TrsB] [GN:trsB] [OR:Staphylococcus aureus] [DB:pir2] >gp: [GI:g310609] [LN:STATRSC] [AC:L11998] [GN:trsB] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus (individual\_isolate pG01) DNA] [DB:genpept-bct1] [DE:Staphylococcus aureus conjugative transfer gene complex (trs).] [NT:putative] [LE:1512] [RE:1829] [DI:direct] >gp: [GI:g3676436] [LN:AF051917] [AC:AF051917:L19570] [PN:putative membrane protein TraB] [GN:traB] [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus plasmid pSK41, complete sequence.] [LE:25115] [RE:25432] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503012391\_5314202\_c3\_219

3757 7529 918 305 1524 2.4e-156

Description

pir: [LN:D56976] [AC:D56976] [PN:transfer complex protein TrsL] [GN:trsL] [OR:Staphylococcus aureus] [DB:pir2] >gp: [GI:g310619] [LN:STATRSC] [AC:L11998] [GN:trsL] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus (individual\_isolate pG01) DNA] [DB:genpept-bct1] [DE:Staphylococcus aureus conjugative transfer gene complex (trs).] [NT:putative] [LE:12193] [RE:13110] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503012391\_6929686\_c1\_152

3758 7530 693 230 1199 6.5e-122

Description

gp: [GI:g1762100] [LN:SEU40385] [AC:U40385] [PN:transposase] [GN:tnp] [OR:Staphylococcus epidermidis] [DB:genpept-bct1] [DE:Staphylococcus epidermidis plasmid pSK818 insertion sequenceIS257(818B) putative transposase gene, complete cds.] [NT:Tnp; putative transposase] [LE:57] [RE:731] [DI:direct] >gp: [GI:g1762102] [LN:SEU40386] [AC:U40386] [PN:transposase] [GN:tnp] [OR:Staphylococcus epidermidis] [DB:genpept-bct1] [DE:Staphylococcus epidermidis plasmid pSK818 insertion sequenceIS257(818C) putative transposase gene, complete cds.] [NT:Tnp; putative transposase] [LE:57] [RE:731] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503012391_6929686_c1_163	3759	7531	693	230	1201	4.0e-122
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Description

pir: [LN:A60634] [AC:A60634:C30471:S26349] [PN:probable transposase] [OR:Staphylococcus aureus] [DB:pir2] >gp: [GI:g46597] [LN:SAIS2571] [AC:X53952] [PN:transposase] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:S.aureus plasmid pSH6 DNA for insertion sequences IS257-1 andIS256.] [LE:188] [RE:862] [DI:direct] >gp: [GI:g3676452] [LN:AF051917] [AC:AF051917:L19570] [PN:putative transposase TnpE] [GN:tnpE] [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus plasmid pSK41, complete sequence.] [LE:40946] [RE:41620] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503012391_6929686_c1_168	3760	7532	693	230	1205	1.5e-122
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Description

pir: [LN:C60634] [AC:C60634:S26351] [PN:probable transposase] [OR:Staphylococcus aureus] [DB:pir2] >gp: [GI:g46600] [LN:SAIS2572] [AC:X53951] [PN:putative transposase] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:S.aureus plasmid pSH6 DNA for insertion sequences IS257-2, IS257-3and IS256.] [LE:1752] [RE:2426] [DI:direct] >gp: [GI:g3676456] [LN:AF051917] [AC:AF051917:L19570] [PN:putative transposase TnpG] [GN:tnpG] [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus plasmid pSK41, complete sequence.] [LE:45713] [RE:46387] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503012391_6929686_c2_197	3761	7533	660	219	1116	4.1e-113
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Description

pir: [LN:A60634] [AC:A60634:C30471:S26349] [PN:probable transposase] [OR:Staphylococcus aureus] [DB:pir2] >gp: [GI:g46597] [LN:SAIS2571] [AC:X53952] [PN:transposase] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:S.aureus plasmid pSH6 DNA for insertion sequences IS257-1 andIS256.] [LE:188] [RE:862] [DI:direct] >gp: [GI:g3676452] [LN:AF051917] [AC:AF051917:L19570] [PN:putative transposase TnpE] [GN:tnpE] [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus plasmid pSK41, complete sequence.] [LE:40946] [RE:41620] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AI7503012391_6929686_c3_229	3762	7534	693	230	1201	4.0e-122
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Description

pir: [LN:A60634] [AC:A60634:C30471:S26349] [PN:probable transposase] [OR:Staphylococcus aureus] [DB:pir2] >gp: [GI:g46597] [LN:SAIS2571] [AC:X53952] [PN:transposase] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:S.aureus plasmid pSH6 DNA for insertion sequences IS257-1 andIS256.] [LE:188] [RE:862] [DI:direct] >gp: [GI:g3676452] [LN:AF051917] [AC:AF051917:L19570] [PN:putative transposase TnpE] [GN:tnpE] [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus plasmid pSK41, complete sequence.] [LE:40946] [RE:41620] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503012391_6929686_f3_115	3763	7535	684	227	1196	1.4e-121
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Description

pir: [LN:B60634] [AC:B60634:S26350] [PN:probable transposase] [OR:Staphylococcus aureus] [DB:pir2] >gp: [GI:g46599] [LN:SAIS2572] [AC:X53951] [PN:putative transposase] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:S.aureus plasmid pSH6 DNA for insertion sequences IS257-2, IS257-3 and IS256.] [LE:556] [RE:1221] [DI:complement] >gp: [GI:g3676455] [LN:AF051917] [AC:AF051917:L19570] [PN:putative transposase TnpF] [GN:tnpF] [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus plasmid pSK41, complete sequence.] [LE:44517] [RE:45182] [DI:complement]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503012391_822802_c3_213	3764	7536	1011	336	1647	2.2e-169
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Description

gp: [GI:g3676426] [LN:AF051917] [AC:AF051917:L19570] [PN:putative replication initiation protein Rep] [GN:rep] [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus plasmid pSK41, complete sequence.] [LE:13205] [RE:14164] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503012392_1442583_c1_19	3765	7537	144	47		
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503012392_1442583_c3_25	3766	7538	144	47		
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503012392_23671885_c1_18	3767	7539	159	52		
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503012392_2776391_f3_12	3768	7540	207	68		
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503012392_29323431_f3_15	3769	7541	123	40		
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
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AT7503012392_30495306_f2_6	3770	7542	123	40		
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503012392_34023375_c2_23	3771	7543	501	166	790	1.4e-78

#### Description

sp: [LN:REMA\_STAAU] [AC:P13969] [GN:REPL:REP] [OR:STAPHYLOCOCCUS AUREUS:STAPHYLOCOCCUS SIMULANS] [DE:REPLICATION AND MAINTENANCE PROTEIN (PLASMID REPLICATION PROTEIN)] [SP:P13969] [DB:swissprot] >pir: [LN:A29827] [AC:A29827:C46568] [PN:replication protein REP] [OR:Staphylococcus aureus] [DB:pir2] >gp: [GI:g153064] [LN:PE5PE5A] [AC:M17990] [GN:repL] [OR:Plasmid pE5] [SR:Plasmid pE5 DNA] [DB:genpept-bct1] [DE:Plasmid pE5 (from Staphylococcus aureus, strain RN451) repL protein and ermC protein, complete cds.] [LE:389] [RE:865] [DI:direct] >gp: [GI:g506624] [LN:STAPTA48CG] [AC:M19652] [OR:Plasmid pT48] [SR:Plasmid pT48 (from S.aureus strain T48) DNA] [DB:genpept-bct1] [DE:Plasmid pT48 (from S.aureus strain T48) complete genome.] [NT:putative. ORF B.] [LE:64] [RE:540] [DI:complement] >gp: [GI:g2407672] [LN:AF019140] [AC:AF019140] [PN:Rep] [GN:rep] [OR:Staphylococcus simulans] [DB:genpept-bct2] [DE:Staphylococcus simulans erythromycin resistance plasmid pPV142 rRNAN-6-methyltransferase (ermM) and replication protein (rep) genes, complete cds.] [NT:plasmid replication protein] [LE:1699] [RE:2175] [DI:direct] >gp: [GI:g1791222] [LN:SCU82607] [AC:U82607] [PN:plasmid replication protein] [OR:Staphylococcus chromogenes] [DB:genpept-bct2] [DE:Staphylococcus chromogenes plasmid pPV141 erythromycin resistance plasmid, rRNA N-6-methyltransferase (ermM) and plasmid replication protein genes, complete cds.] [LE:1583] [RE:2059] [DI:direct]

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>score</u>	<u>probability</u>
AI7503012392_4304683_c2_21	3772	7544	771	256	1270	2.0e-129

#### Description

sp: [LN:ERM4\_STAAU] [AC:P13978] [GN:ERMC] [OR:STAPHYLOCOCCUS AUREUS] [EC:2.1.1.48] [DE:RESISTANCE PROTEIN] [SP:P13978] [DB:swissprot] >pir: [LN:B46568] [AC:B46568] [PN:ermC protein] [CL:rRNA (adenine-N6-) -methyltransferase] [OR:Staphylococcus aureus] [DB:pir2] >gp: [GI:g455358] [LN:STAPTA48CG] [AC:M19652] [PN:23S RNA methylase] [GN:ermC] [OR:Plasmid pT48] [SR:Plasmid pT48 (from S.aureus strain T48) DNA] [DB:genpept-bct1] [DE:Plasmid pT48 (from S.aureus strain T48) complete genome.] [LE:988] [RE:1722] [DI:complement]